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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

FIRST-NAMED INVENTOR OR  
APPLICATION IDENTIFIER: Richard A. Shimkets

FOR: **NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE  
POLYMORPHISMS AND METHODS OF USE THEREOF**

November 22, 2000

Boston, Massachusetts

Box PATENT APPLICATION  
Assistant Commissioner for Patents  
Washington, D.C. 20231

**REQUEST FOR FILING A NEW NONPROVISIONAL APPLICATION  
UNDER 37 C.F.R. §1.53(b)**

1. This is a request for filing a new nonprovisional application under 37 C.F.R. §1.53(b).
2. ☒ Specification and Drawings (Total pages: 682);  
Specification (50 pages); Claims (10 pages); Abstract (1 page); Sequence Listing  
(431 pages); and Table 1 (190 pages).
3. ☒ Declaration and Power of Attorney  
☒ Unsigned  
☐ Signed
4. ☐ Information Disclosure Statement (IDS)  
☐ Copy of IDS and PTO-1449 (\_\_\_ pages)  
☐ Copies of references cited
5. ☐ Assignment Papers  
☐ Recordation Form Cover Sheet (PTO-1595)  
☐ Assignment Document
6. ☐ Statement Claiming Small Entity Status  
☐ Claiming Small Entity As Independent Inventor (37 C.F.R. §§1.9(f) & 1.27(b)).  
☐ Claiming Small Entity As Small Business Concern (37 C.F.R. §§1.9(f) & 1.27(c)).  
☐ Claiming Small Entity As Nonprofit Organization (37 C.F.R. §§1.9(f) & 1.27(d)).

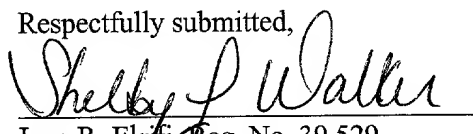
FIRST-NAMED INVENTOR OR      **Richard A. Shimkets**  
APPLICATION IDENTIFIER:  
Request for New Nonprovisional Application (37 C.F.R. §1.53(b))

7. Fee Calculation

| CLAIMS AS FILED  |                 |                        |                 |  |   |
|--|-----------------|------------------------|-----------------|--|---|
| Claims   | Number<br>Filed | Basic Fee<br>Allowance | Number<br>Extra | Rate   | Basic Fee<br>37 C.F.R. 1.16(a)<br>\$ 710.00 |
| Total Claims (37 C.F.R. 1.16(c))                           | 44              | - 20 =                 | 24              | \$ 18.00                                     | \$ 432.00                                   |
| Independent Claims (37 C.F.R. 1.16(b))                     | 11              | - 3 =                  | 8               | \$ 80.00                                     | \$ 640.00                                   |
| Multiple Dependent Claim(s), if any<br>(37 C.F.R. 1.16(d)) |                 |                        |                 | \$260.00                                     | 0   |
|  |                 |                        |                 | SUBTOTAL:                                    | \$1,782.00                                  |
|  |                 |                        |                 | Reduction by 50% for filing by small entity: | 891.00                                      |
|  |                 |                        |                 | <b>TOTAL FEE:</b>                            | <b>\$891.00</b>                             |

8. ☒ A check in the amount of **\$891.00** is enclosed.
9. ☒ The Commissioner is hereby authorized to credit overpayments or charge the following fees to Deposit Account No. 50-0311, Ref. No. 15966-565 (CURA-65):
- ☒ Fees required under 37 C.F.R. §1.16;  
☒ Fees required under 37 C.F.R. §1.17;  
☒ Fees required under 37 C.F.R. §1.18.
10. ☒ Return Receipt Postcard Enclosed.
11. ☐ Other Documents Enclosed:
- ☐ Change of Attorney Address In Application.  
☐ Limited Recognition under 37 C.F. § 10.9(b) for Michel Morency.

Respectfully submitted,



Dated: November 22, 2000

Ivor R. Elrifi, Reg. No. 39,529  
Shelby J. Walker, Reg. No. 45, 192  
Attorney(s) for Applicants  
MINTZ, LEVIN, COHN, FERRIS,  
GLOVSKY and POPEO, P.C.  
One Financial Center  
Boston, Massachusetts 02111  
Tel: (617) 542-6000  
Fax: (617) 542-2241

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# NUCLEIC ACIDS CONTAINING SINGLE NUCLEOTIDE POLYMORPHISMS AND METHODS OF USE THEREOF

## RELATED APPLICATIONS

This application claims priority to U.S.S.N. 60/167,383, filed November 24, 1999, which is incorporated herein by reference in its entirety.

## BACKGROUND OF THE INVENTION

Sequence polymorphism-based analysis of nucleic acid sequences can augment or replace previously known methods for determining the identity and relatedness of individuals. The approach is generally based on alterations in nucleic acid sequences between related individuals. This analysis has been widely used in a variety of genetic, diagnostic, and forensic applications. For example, polymorphism analyses are used in identity and paternity analysis, and in genetic mapping studies.

One such type of variation is a restriction fragment length polymorphism (RFLP). RFLPS can create or delete a recognition sequence for a restriction endonuclease in one nucleic acid relative to a second nucleic acid. The result of the variation is an alteration in the relative length of restriction enzyme generated DNA fragments in the two nucleic acids.

Other polymorphisms take the form of short tandem repeats (STR) sequences, which are also referred to as variable numbers of tandem repeat (VNTR) sequences. STR sequences typically that include tandem repeats of 2, 3, or 4 nucleotide sequences that are present in a nucleic acid from one individual but absent from a second, related individual at the corresponding genomic location.

Other polymorphisms take the form of single nucleotide variations, termed single nucleotide polymorphisms (SNPs), between individuals. A SNP can, in some instances, be referred to as a "cSNP" to denote that the nucleotide sequence containing the SNP

originates as a cDNA.

SNPs can arise in several ways. A single nucleotide polymorphism may arise due to a substitution of one nucleotide for another at the polymorphic site. Substitutions can be transitions or transversions. A transition is the replacement of one purine nucleotide by another purine nucleotide, or one pyrimidine by another pyrimidine. A transversion is the replacement of a purine by a pyrimidine, or the converse.

Single nucleotide polymorphisms can also arise from a deletion of a nucleotide or an insertion of a nucleotide relative to a reference allele. Thus, the polymorphic site is a site at which one allele bears a gap with respect to a single nucleotide in another allele.

Some SNPs occur within, or near genes. One such class includes SNPs falling within regions of genes encoding for a polypeptide product. These SNPs may result in an alteration of the amino acid sequence of the polypeptide product and give rise to the expression of a defective or other variant protein. Such variant products can, in some cases result in a pathological condition, *e.g.*, genetic disease. Examples of genes in which a polymorphism within a coding sequence gives rise to genetic disease include sickle cell anemia and cystic fibrosis. Other SNPs do not result in alteration of the polypeptide product. Of course, SNPs can also occur in noncoding regions of genes.

SNPs tend to occur with great frequency and are spaced uniformly throughout the genome. The frequency and uniformity of SNPs means that there is a greater probability that such a polymorphism will be found in close proximity to a genetic locus of interest.

#### SUMMARY OF THE INVENTION

The invention is based in part on the discovery of novel single nucleotide polymorphisms (SNPs) in regions of human DNA.

Accordingly, in one aspect, the invention provides an isolated polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 1468) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it

includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS: 1-1468), or a fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

5           The polynucleotide can be, *e.g.*, DNA or RNA, and can be between about 10 and about 100 nucleotides, *e.g.* 10-90, 10-75, 10-51, 10-40, or 10-30, nucleotides in length.

          In some embodiments, the polymorphic site in the polymorphic sequence includes a nucleotide other than the nucleotide listed in Table 1, column 5 for the polymorphic sequence, *e.g.*, the polymorphic site includes the nucleotide listed in Table 1, column 6  
10       for the polymorphic sequence.

          In other embodiments, the complement of the polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of the polymorphic sequence, *e.g.*, the complement of the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

15           In some embodiments, the polymorphic sequence is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated with a polypeptide related to an ATPase associated protein, a cadherin, or any of the other proteins identified in Table 1, column 10.

          In another aspect, the invention provides an isolated allele-specific  
20       oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide  
25       sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the complementary nucleotide

sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

5 In some embodiments, the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide. The second polynucleotide can be, *e.g.*, (a) a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), wherein the polymorphic sequence includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence; (b) a nucleotide sequence that is a fragment of  
10 any of the polymorphic sequences; (c) a complementary nucleotide sequence including a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), wherein the polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and (d) a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the  
15 polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The invention also provides a method of detecting a polymorphic site in a nucleic  
20 acid. The method includes contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the  
25 nucleotide recited in Table 1, column 5. The method also includes determining whether the nucleic acid and the oligonucleotide hybridize. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphic site in the nucleic acid.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

In some embodiments, the polymorphic sequence identified by the oligonucleotide is associated with a polypeptide related to one of the protein families disclosed herein. For example, the nucleic acid may be associated polypeptide related to an ATPase associated protein, cadherin, or any of the other protein families identified in Table 1, column 10.

In another aspect, the method includes determining if a sequence polymorphism is the present in a subject, such as a human. The method includes providing a nucleic acid from the subject and contacting the nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. Hybridization between the nucleic acid and the oligonucleotide is then determined. Hybridization of the oligonucleotide to the nucleic acid sequence indicates the presence of the polymorphism in said subject.

In a further aspect, the invention provides a method of determining the relatedness of a first and second nucleic acid. The method includes providing a first nucleic acid and a second nucleic acid and contacting the first nucleic acid and the second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1,

column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The method also includes determining whether the first nucleic acid and the second nucleic acid hybridize to the oligonucleotide, and comparing hybridization of the first and second nucleic acids to the oligonucleotide. Hybridization of first and second nucleic acids to the nucleic acid indicates the first and second subjects are related.

In preferred embodiments, the oligonucleotide does not hybridize to the polymorphic sequence when the polymorphic sequence includes the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for the polymorphic sequence.

The oligonucleotide can be, *e.g.*, between about 10 and about 100 bases in length. In some embodiments, the oligonucleotide is between about 10 and 75 bases, 10 and 51 bases, 10 and about 40 bases, or about 15 and 30 bases in length.

The method can be used in a variety of applications. For example, the first nucleic acid may be isolated from physical evidence gathered at a crime scene, and the second nucleic acid may be obtained from a person suspected of having committed the crime. Matching the two nucleic acids using the method can establish whether the physical evidence originated from the person.

In another example, the first sample may be from a human male suspected of being the father of a child and the second sample may be from the child. Establishing a match using the described method can establish whether the male is the father of the child.

In another aspect, the invention provides an isolated polypeptide comprising a polymorphic site at one or more amino acid residues, and wherein the protein is encoded by a polynucleotide including one of the polymorphic sequences SEQ ID NOS:1-1468, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the

complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

The polypeptide can be, *e.g.*, related to one of the protein families disclosed herein. For example, polypeptide can be related to an ATPase associated protein, cadherin, or any of the other proteins provided in Table 1, column 10.

In some embodiments, the polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

In some embodiments, the polypeptide encoded by the polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

The invention also provides an antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-1468, or its complement. The polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

In some embodiments, the antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

Preferably, the antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for the polymorphic sequence.

The invention further provides a method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject. The

method includes providing a protein sample from the subject and contacting the sample with the above-described antibody under conditions that allow for the formation of antibody-antigen complexes. The antibody-antigen complexes are then detected. The presence of the complexes indicates the presence of the polypeptide.

5           The invention also provides a method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, *e.g.*, a human, non-human primate, cat, dog, rat, mouse, cow, pig, goat, or rabbit. The method includes providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic  
10   sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or its complement, and treating the subject by administering to the subject an effective dose of a therapeutic agent. Aberrant expression can include qualitative alterations in expression of a gene, *e.g.*, expression of a gene encoding a polypeptide having an altered amino acid sequence with respect to its wild-type counterpart. Qualitatively different polypeptides  
15   can include, shorter, longer, or altered polypeptides relative to the amino acid sequence of the wild-type polypeptide. Aberrant expression can also include quantitative alterations in expression of a gene. Examples of quantitative alterations in gene expression include lower or higher levels of expression of the gene relative to its wild-type counterpart, or alterations in the temporal or tissue-specific expression pattern of a gene. Finally,  
20   aberrant expression may also include a combination of qualitative and quantitative alterations in gene expression.

The therapeutic agent can include, *e.g.*, second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele. In some embodiments, the second nucleic acid sequence  
25   comprises a polymorphic sequence which includes nucleotide listed in Table 1, column 5 for the polymorphic sequence.

Alternatively, the therapeutic agent can be a polypeptide encoded by a polynucleotide comprising polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is



complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 6 for the polymorphic sequence.

The therapeutic agent may further include an antibody as herein described, or an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that the polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for the polymorphic sequence.

In another aspect, the invention provides an oligonucleotide array comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468); a nucleotide sequence that is a fragment of any of the nucleotide sequences, provided that the fragment includes a polymorphic site in the polymorphic sequence; a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468); or a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

In preferred embodiments, the array comprises 10; 100; 1,000; 10,000; 100,000 or more oligonucleotides.

The invention also provides a kit comprising one or more of the herein-described nucleic acids. The kit can include, *e.g.*, a polynucleotide which includes one or more of the SNPs described herein. The polynucleotide can be, *e.g.*, a nucleotide sequence which includes one or more of the polymorphic sequences shown in Table 1 and the Sequence Listing (SEQ ID NOS: 1 - 1468) and which includes a polymorphic sequence, or a fragment of the polymorphic sequence, as long as it includes the polymorphic site. The polynucleotide may alternatively contain a nucleotide sequence which includes a sequence complementary to one or more of the sequences (SEQ ID NOS:1-1468), or a

fragment of the complementary nucleotide sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence. The invention provides an isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide containing a polymorphic site. The first polynucleotide can be, *e.g.*, a nucleotide sequence comprising one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for the polymorphic sequence. Alternatively, the first polynucleotide can be a nucleotide sequence that is a fragment of the polymorphic sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence, or a complementary nucleotide sequence which includes a sequence complementary to one or more polymorphic sequences (SEQ ID NOS:1 - 1468), provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5. The first polynucleotide may in addition include a nucleotide sequence that is a fragment of the complementary sequence, provided that the fragment includes a polymorphic site in the polymorphic sequence.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

## DETAILED DESCRIPTION OF THE INVENTION

The invention provides human SNPs in sequences which are transcribed, *i.e.*, are cSNPs. As is explained in more detail below, many SNPs have been identified in genes related to polypeptides of known function. For some applications, SNPs associated with various polypeptides can be used together. For example, SNPs can be group according to whether they are derived from a nucleic acid encoding a polypeptide related to a particular protein family or involved in a particular function. Thus, SNPs related to ATPase associated protein may be collected for some applications, as may SNPs associated with cadherin, or ephrin (EPH), or any of the other proteins recited in Table 1, column 10. Similarly, SNPs can be grouped according to the functions played by their gene products. Such functions include, e.g., structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism.

The SNPs are shown in Table 1 and the Sequence Listing. Both provide a summary of the polymorphic sequences disclosed herein. In the Table, a “SNP” is a polymorphic site embedded in a polymorphic sequence. The polymorphic site is occupied by a single nucleotide, which is the position of nucleotide variation between the wild type and polymorphic allelic sequences. The site is usually preceded by and followed by relatively highly conserved sequences of the allele (e.g., sequences that vary in less than 1/100 or 1/1000 members of the populations). Thus, a polymorphic sequence can include one or more of the following sequences: (1) a sequence having the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence; or (2) a sequence having a nucleotide other than the nucleotide denoted in Table 1, column 5 at the polymorphic site in the polymorphic sequence. An example of the latter sequence is a polymorphic sequence having the nucleotide denoted in Table 1, column 6 at the polymorphic site in the polymorphic sequence.

Nucleotide sequences for a referenced-polymorphic pair are presented in Table 1. Each cSNP entry provides information concerning the wild type nucleotide sequence as well as the corresponding sequence that includes the SNP at the polymorphic site. Since

the wild type sequence is already known, the Sequence Listing accompanying this application provides only the sequence of the polymorphic allele; its SEQ ID NO: is also cross referenced in the Table 1. A reference to the SEQ ID NO: giving the translated amino acid sequence is also given if appropriate. The Table includes thirteen columns that provide descriptive information for each cSNP, each of which occupies one row in the Table. The column headings, and an explanation for each, are given below.

“SEQ ID” provides the cross-reference to the nucleotide SEQ ID NO:, and, as explained below, an amino acid SEQ ID NO: as well, in the Sequence Listing of the application. Conversely, each sequence entry in the Sequence Listing also includes a cross-reference to the CuraGen sequence ID, under the label “CuraGen Sequence ID”. The first SEQ ID NO: given in the first column of each row of the Table is the SEQ ID NO: identifying the nucleic acid sequence for the polymorphism. If a polymorphism carries an entry for the amino acid portion of the row, a second SEQ ID NO: appears in parentheses in the column “Amino acid after” (see below). This second SEQ ID NO: refers to an amino acid sequence giving the polymorphic amino acid sequence that is the translation of the nucleotide polymorphism. If a polymorphism carries no entry for the protein portion of the row, only one SEQ ID NO: is provided.

“CuraGen sequence ID” provides CuraGen Corporation’s accession number.

“Base pos. of SNP” gives the numerical position of the nucleotide in the reference, or wild-type, gene at which the cSNP is found. This enumeration of bases is that found in the public database from which the reference gene is taken (see column headed “Name of protein identified following a BLASTX analysis of the CuraGen sequence”) as of the filing date of the instant application.

“Polymorphic sequence” provides a 51-base sequence with the polymorphic site at the 26<sup>th</sup> base in the sequence, as well as 25 bases from the reference sequence on the 5’ side and the 3’ side of the polymorphic site. The designation at the polymorphic site is enclosed in square brackets, and provides first, the reference nucleotide; second, a “slash (/)”; and third, the polymorphic nucleotide. In certain cases the polymorphism is an

insertion or a deletion. In that case, the position which is “unfilled” (i.e., the reference or the polymorphic position) is indicated by the word “gap”.

“Base before” provides the nucleotide present in the reference, or wild-type, gene at the position at which the polymorphism is found.

5 “Base after” provides the altered nucleotide at the position of the polymorphism.

“Amino acid before” provides the amino acid in the reference protein, if the polymorphism occurs in a coding region.

10 “Amino acid after” provides the amino acid in the polymorphic protein, if the polymorphism occurs in a coding region. This column also includes the SEQ ID NO: in parentheses if the polymorphism occurs in a coding region.

“Type of change” provides information on the nature of the polymorphism.

“SILENT-NONCODING” is used if the polymorphism occurs in a noncoding region of a nucleic acid.

15 “SILENT-CODING” is used if the polymorphism occurs in a coding region of a nucleic acid of a nucleic acid and results in no change of amino acid in the translated polymorphic protein.

“CONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in the same class as the reference amino acid. The classes are:

20 Aliphatic: Gly, Ala, Val, Leu, Ile;

Aromatic: Phe, Tyr, Trp;

Sulfur-containing: Cys, Met;

Aliphatic OH: Ser, Thr;

Basic: Lys, Arg, His;

Acidic: Asp, Glu, Asn, Gln;

Pro falls in none of the other classes; and

End defines a termination codon.

5 “NONCONSERVATIVE” is used if the polymorphism occurs in a coding region of a nucleic acid and provides a change in which the altered amino acid falls in a different class than the reference amino acid.

“FRAMESHIFT” relates to an insertion or a deletion. If the frameshift occurs in a coding region, the Table provides the translation of the frameshifted codons 3’ to the polymorphic site.

10 “Protein classification of CuraGen gene” provides a generic class into which the protein is classified. During the course of the work leading to the filing of this application, several classes of proteins were identified. Some are described further below.

15 “Name of protein identified following a BLASTX analysis of the CuraGen sequence” provides the database reference for the protein found to resemble the novel reference-polymorphism cognate pair most closely.

20 “Similarity (pvalue) following a BLASTX analysis” provides the pvalue, a statistical measure from the BLASTX analysis that the polymorphic sequence is similar to, and therefore an allele of, the reference, or wild-type, sequence. In the present application, a cutoff of  $pvalue > 1 \times 10^{-50}$  (entered, for example, as 1.0E-50 in the Table) is used to establish that the reference-polymorphic cognate pairs are novel. A  $pvalue < 1 \times 10^{-50}$  defines proteins considered to be already known.

“Map location” provides any information available at the time of filing related to localization of a gene on a chromosome.

25 The polymorphisms are arranged in the Table in the following order.

SEQ ID NOs: 1-722 are SNPs that are silent.

SEQ ID NOs: 723-797 are SNPs that lead to conservative amino acid changes.

SEQ ID NOs: 798-989 are SNPs that lead to nonconservative amino acid changes.

5        SEQ ID NOs: 990-1095 are SNPs that involve a gap. With respect to the reference or wild-type sequence at the position of the polymorphism, the allelic cSNP introduces an additional nucleotide (an insertion) or deletes a nucleotide (a deletion). An SNP that involves a gap generates a frame shift.

10        SEQ ID NOs: 1096-1170 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to conservative amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 723-797. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

15        SEQ ID NOs: 1171-1362 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to nonconservative amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 798-989. 7 or 8 amino acids on either side of the polymorphic site are shown. The order in which these sequences appear mirrors the  
20        order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

      SEQ ID NOs: 1363-1468 are the amino acid sequences centered at the polymorphic amino acid residue for the protein products provided by SNPs that lead to frameshift-induced amino acid changes. These amino acid SEQ ID NOs: are derived from the corresponding nucleotide SEQ ID NOs: 990-1095. 7 or 8 amino acids on either  
25        side of the polymorphic site are shown. The order in which these sequences appear mirrors the order of presentation of the cognate nucleotide sequences, and is set forth in the Table.

Provided herein are compositions which include, or are capable of detecting, nucleic acid sequences having these polymorphisms, as well as methods of using nucleic acids.

#### IDENTIFICATION OF INDIVIDUALS CARRYING SNPs

5 Individuals carrying polymorphic alleles of the invention may be detected at either the DNA, the RNA, or the protein level using a variety of techniques that are well known in the art. Strategies for identification and detection are described in *e.g.*, EP 730,663, EP 717,113, and PCT US97/02102. The present methods usually employ pre-characterized polymorphisms. That is, the genotyping location and nature of  
10 polymorphic forms present at a site have already been determined. The availability of this information allows sets of probes to be designed for specific identification of the known polymorphic forms.

Many of the methods described below require amplification of DNA from target samples. This can be accomplished by *e.g.*, PCR. See generally PCR Technology:  
15 Principles and Applications for DNA Amplification (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); PCR Protocols: A Guide to Methods and Applications (eds. Innis, et al., Academic Press, San Diego, CA, 1990); Mattila et al., Nucleic Acids Res. 19, 4967 (1991); Eckert et al., PCR Methods and Applications 1, 17 (1991); PCR (eds. McPherson et al., IRL Press, Oxford); and U.S. Patent 4,683,202.

20 The phrase "recombinant protein" or "recombinantly produced protein" refers to a peptide or protein produced using non-native cells that do not have an endogenous copy of DNA able to express the protein. In particular, as used herein, a recombinantly produced protein relates to the gene product of a polymorphic allele, *i.e.*, a "polymorphic protein" containing an altered amino acid at the site of translation of the nucleotide  
25 polymorphism. The cells produce the protein because they have been genetically altered by the introduction of the appropriate nucleic acid sequence. The recombinant protein will not be found in association with proteins and other subcellular components normally associated with the cells producing the protein. The terms "protein" and "polypeptide" are used interchangeably herein.



The phrase "substantially purified" or "isolated" when referring to a nucleic acid, peptide or protein, means that the chemical composition is in a milieu containing fewer, or preferably, essentially none, of other cellular components with which it is naturally associated. Thus, the phrase "isolated" or "substantially pure" refers to nucleic acid preparations that lack at least one protein or nucleic acid normally associated with the nucleic acid in a host cell. It is preferably in a homogeneous state although it can be in either a dry or aqueous solution. Purity and homogeneity are typically determined using analytical chemistry techniques such as gel electrophoresis or high performance liquid chromatography. Generally, a substantially purified or isolated nucleic acid or protein will comprise more than 80% of all macromolecular species present in the preparation. Preferably, the nucleic acid or protein is purified to represent greater than 90% of all macromolecular species present. More preferably the nucleic acid or protein is purified to greater than 95%, and most preferably the nucleic acid or protein is purified to essential homogeneity, wherein other macromolecular species are not detected by conventional analytical procedures.

The genomic DNA used for the diagnosis may be obtained from any nucleated cells of the body, such as those present in peripheral blood, urine, saliva, buccal samples, surgical specimen, and autopsy specimens. The DNA may be used directly or may be amplified enzymatically in vitro through use of PCR (Saiki et al. Science 239:487-491 (1988)) or other in vitro amplification methods such as the ligase chain reaction (LCR) (Wu and Wallace Genomics 4:560-569 (1989)), strand displacement amplification (SDA) (Walker et al. Proc. Natl. Acad. Sci. U.S.A. 89:392-396 (1992)), self-sustained sequence replication (3SR) (Fahy et al. PCR Methods P&J 1:25-33 (1992)), prior to mutation analysis.

The method for preparing nucleic acids in a form that is suitable for mutation detection is well known in the art. A "nucleic acid" is a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, including known analogs of natural nucleotides unless otherwise indicated. The term "nucleic acids", as used herein, refers to either DNA or RNA. "Nucleic acid sequence" or "polynucleotide sequence" refers to a single-stranded sequence of deoxyribonucleotide or ribonucleotide

bases read from the 5' end to the 3' end. The direction of 5' to 3' addition of nascent RNA transcripts is referred to as the transcription direction; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 5' end of the RNA transcript in the 5' direction are referred to as "upstream sequences"; sequence regions on the DNA strand having the same sequence as the RNA and which are beyond the 3' end of the RNA transcript in the 3' direction are referred to as "downstream sequences". The term includes both self-replicating plasmids, infectious polymers of DNA or RNA and nonfunctional DNA or RNA. The complement of any nucleic acid sequence of the invention is understood to be included in the definition of that sequence.

10 "Nucleic acid probes" may be DNA or RNA fragments.

The detection of polymorphisms in specific DNA sequences, can be accomplished by a variety of methods including, but not limited to, restriction-fragment-length-polymorphism detection based on allele-specific restriction-endonuclease cleavage (Kan and Dozy Lancet ii:910-912 (1978)), hybridization with allele-specific oligonucleotide probes (Wallace et al. Nucl. Acids Res. 6:3543-3557 (1978)), including immobilized oligonucleotides (Saiki et al. Proc. Natl. Acad. Sci. USA, 86:6230-6234 (1989)) or oligonucleotide arrays (Maskos and Southern Nucl. Acids Res 21:2269-2270 (1993)), allele-specific PCR (Newton et al. Nucl Acids Res 17:2503-2516 (1989)), mismatch-repair detection (MRD) (Faham and Cox Genome Res 5:474-482 (1995)), binding of MutS protein (Wagner et al. Nucl Acids Res 23:3944-3948 (1995)), denaturing-gradient gel electrophoresis (DGGE) (Fisher and Lerman et al. Proc. Natl. Acad. Sci. U.S.A. 80:1579-1583 (1983)), single-strand-conformation-polymorphism detection (Orita et al. Genomics 5:874-879 (1983)), RNAase cleavage at mismatched base-pairs (Myers et al. Science 230:1242 (1985)), chemical (Cotton et al. Proc. Natl. w Sci. U.S.A. 8Z4397-4401 (1988)) or enzymatic (Youil et al. Proc. Natl. Acad. Sci. U.S.A. 92:87-91 (1995)) cleavage of heteroduplex DNA, methods based on allele specific primer extension (Syvanen et al. Genomics 8:684-692 (1990)), genetic bit analysis (GBA) (Nikiforov et al. &&I Acids 22:4167-4175 (1994)), the oligonucleotide-ligation assay (OLA) (Landegren et al. Science 241:1077 (1988)), the allele-specific ligation chain reaction (LCR) (Barrany Proc. Natl. Acad. Sci. U.S.A. 88:189-193 (1991)), gap-LCR (Abravaya et al. Nucl Acids Res 23:675-682 (1995)), radioactive and/or fluorescent

DNA sequencing using standard procedures well known in the art, and peptide nucleic acid (PNA) assays (Orum et al., *Nucl. Acids Res*, 21:5332-5356 (1993); Thiede et al., *Nucl. Acids Res*. 24:983-984 (1996)).

“Specific hybridization” or “selective hybridization” refers to the binding, or duplexing, of a nucleic acid molecule only to a second particular nucleotide sequence to which the nucleic acid is complementary, under suitably stringent conditions when that sequence is present in a complex mixture (e.g., total cellular DNA or RNA). “Stringent conditions” are conditions under which a probe will hybridize to its target subsequence, but to no other sequences. Stringent conditions are sequence-dependent and are different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter ones. Generally, stringent conditions are selected such that the temperature is about 5°C lower than the thermal melting point ( $T_m$ ) for the specific sequence to which hybridization is intended to occur at a defined ionic strength and pH. The  $T_m$  is the temperature (under defined ionic strength, pH, and nucleic acid concentration) at which 50% of the target sequence hybridizes to the complementary probe at equilibrium. Typically, stringent conditions include a salt concentration of at least about 0.01 to about 1.0 M Na ion concentration (or other salts), at pH 7.0 to 8.3. The temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides). Stringent conditions can also be achieved with the addition of destabilizing agents such as formamide. For example, conditions of 5X SSPE (750 mM NaCl, 50 mM NaPhosphate, 5 mM EDTA, pH 7.4) and a temperature of 25-30°C are suitable for allele-specific probe hybridization.

“Complementary” or “target” nucleic acid sequences refer to those nucleic acid sequences which selectively hybridize to a nucleic acid probe. Proper annealing conditions depend, for example, upon a probe’s length, base composition, and the number of mismatches and their position on the probe, and must often be determined empirically. For discussions of nucleic acid probe design and annealing conditions, see, for example, Sambrook et al., or Current Protocols in Molecular Biology, F. Ausubel et al., ed., Greene Publishing and Wiley-Interscience, New York (1987).

A perfectly matched probe has a sequence perfectly complementary to a particular target sequence. The test probe is typically perfectly complementary to a portion of the target sequence. A "polymorphic" marker or site is the locus at which a sequence difference occurs with respect to a reference sequence. Polymorphic markers include restriction fragment length polymorphisms, variable number of tandem repeats (VNTR's), hypervariable regions, minisatellites, dinucleotide repeats, trinucleotide repeats, tetranucleotide repeats, simple sequence repeats, and insertion elements such as Alu. The reference allelic form may be, for example, the most abundant form in a population, or the first allelic form to be identified, and other allelic forms are designated as alternative, variant or polymorphic alleles. The allelic form occurring most frequently in a selected population is sometimes referred to as the "wild type" form, and herein may also be referred to as the "reference" form. Diploid organisms may be homozygous or heterozygous for allelic forms. A diallelic polymorphism has two distinguishable forms (i.e., base sequences), and a triallelic polymorphism has three such forms.

As used herein an "oligonucleotide" is a single-stranded nucleic acid ranging in length from 2 to about 60 bases. Oligonucleotides are often synthetic but can also be produced from naturally occurring polynucleotides. A probe is an oligonucleotide capable of binding to a target nucleic acid of a complementary sequence through one or more types of chemical bonds, usually through complementary base pairing via hydrogen bond formation. Oligonucleotides probes are often between 5 and 60 bases, and, in specific embodiments, may be between 10-40, or 15-30 bases long. An oligonucleotide probe may include natural (i.e. A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in an oligonucleotide probe may be joined by a linkage other than a phosphodiester bond, such as a phosphoramidite linkage or a phosphorothioate linkage, or they may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than by phosphodiester bonds, so long as it does not interfere with hybridization.

As used herein, the term "primer" refers to a single-stranded oligonucleotide which acts as a point of initiation of template-directed DNA synthesis under appropriate conditions (e.g., in the presence of four different nucleoside triphosphates and a

polymerization agent, such as DNA polymerase, RNA polymerase or reverse transcriptase) in an appropriate buffer and at a suitable temperature. The appropriate length of a primer depends on the intended use of the primer, but typically ranges from 15 to 30 nucleotides. Short primer molecules generally require cooler temperatures to form sufficiently stable hybrid complexes with the template. A primer need not be perfectly complementary to the exact sequence of the template, but should be sufficiently complementary to hybridize with it. The term "primer site" refers to the sequence of the target DNA to which a primer hybridizes. The term "primer pair" refers to a set of primers including a 5' (upstream) primer that hybridizes with the 5' end of the DNA sequence to be amplified and a 3' (downstream) primer that hybridizes with the complement of the 3' end of the sequence to be amplified.

DNA fragments can be prepared, for example, by digesting plasmid DNA, or by use of PCR. Oligonucleotides for use as primers or probes are chemically synthesized by methods known in the field of the chemical synthesis of polynucleotides, including by way of non-limiting example the phosphoramidite method described by Beaucage and Carruthers, Tetrahedron Lett 22:1859-1 862 (1981) and the triester method provided by Matteucci, et al., J. Am. Chem. Soc., 103:3185 (1981) both incorporated herein by reference. These syntheses may employ an automated synthesizer, as described in Needham-VanDevanter, D.R., et al., Nucleic Acids Res. 12:61596168 (1984). Purification of oligonucleotides may be carried out by either native acrylamide gel electrophoresis or by anion-exchange HPLC as described in Pearson, J.D. and Regnier, F.E., J. Chrom., 255:137-149 (1983). A double stranded fragment may then be obtained, if desired, by annealing appropriate complementary single strands together under suitable conditions or by synthesizing the complementary strand using a DNA polymerase with an appropriate primer sequence. Where a specific sequence for a nucleic acid probe is given, it is understood that the complementary strand is also identified and included. The complementary strand will work equally well in situations where the target is a double-stranded nucleic acid.

The sequence of the synthetic oligonucleotide or of any nucleic acid fragment can be can be obtained using either the dideoxy chain termination method or the Maxam-

Gilbert method (see Sambrook et al. Molecular Cloning - a Laboratory Manual (2nd Ed.), Vols. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor, New York, (1989), which is incorporated herein by reference. This manual is hereinafter referred to as "Sambrook et al." ; Zyskind et al., (1988)). Recombinant DNA Laboratory Manual, (Acad. Press, New York). Oligonucleotides useful in diagnostic assays are typically at least 8 consecutive nucleotides in length, and may range upwards of 18 nucleotides in length to greater than 100 or more consecutive nucleotides.

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the SNP-containing nucleotide sequences of the invention, or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, about 25, about 50, or about 60 nucleotides or an entire SNP coding strand, or to only a portion thereof.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a polymorphic nucleotide sequence of the invention. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence of the invention. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences disclosed herein, antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. For example, the antisense nucleic acid molecule can generally be complementary to the entire coding region of an mRNA, but more preferably as

embodied herein, it is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of the mRNA. An antisense oligonucleotide can range in length between about 5 and about 60 nucleotides, preferably between about 10 and about 45 nucleotides, more preferably between about 15 and 40 nucleotides, and still more preferably between about 15 and 30 in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following section).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a polymorphic protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementary to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual -u nits, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA -DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

The following terms are used to describe the sequence relationships between two or more nucleic acids or polynucleotides: "reference sequence", "comparison window", "sequence identity", "percentage of sequence identity", and "substantial identity". A "reference sequence" is a defined sequence used as a basis for a sequence comparison; a reference sequence may be a subset of a larger sequence, for example, as a segment of a full-length cDNA or gene sequence given in a sequence listing, or may comprise a



complete cDNA or gene sequence. Optimal alignment of sequences for aligning a comparison window may, for example, be conducted by the local homology algorithm of Smith and Waterman Adv. Appl. Math. 2482 (1981), by the homology alignment algorithm of Needleman and Wunsch J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson and Lipman Proc. Natl. Acad. Sci. U.S.A. 852444 (1988), or by computerized implementations of these algorithms (for example, GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package Release 7.0, Genetics Computer Group, 575 Science Dr., Madison, WI).

Techniques for nucleic acid manipulation of the nucleic acid sequences harboring the cSNP's of the invention, such as subcloning nucleic acid sequences encoding polypeptides into expression vectors, labeling probes, DNA hybridization, and the like, are described generally in Sambrook et al., The phrase "nucleic acid sequence encoding" refers to a nucleic acid which directs the expression of a specific protein, peptide or amino acid sequence. The nucleic acid sequences include both the DNA strand sequence that is transcribed into RNA and the RNA sequence that is translated into protein, peptide or amino acid sequence. The nucleic acid sequences include both the full length nucleic acid sequences disclosed herein as well as non-full length sequences derived from the full length protein. It being further understood that the sequence includes the degenerate codons of the native sequence or sequences which may be introduced to provide codon preference in a specific host cell. Consequently, the principles of probe selection and array design can readily be extended to analyze more complex polymorphisms (see EP 730,663). For example, to characterize a triallelic SNP polymorphism, three groups of probes can be designed tiled on the three polymorphic forms as described above. As a further example, to analyze a diallelic polymorphism involving a deletion of a nucleotide, one can tile a first group of probes based on the undeleted polymorphic form as the reference sequence and a second group of probes based on the deleted form as the reference sequence.

For assay of genomic DNA, virtually any biological convenient tissue sample can be used. Suitable samples include whole blood, semen, saliva, tears, urine, fecal material, sweat, buccal, skin and hair can be used. Genomic DNA is typically amplified before

analysis. Amplification is usually effected by PCR using primers flanking a suitable fragment e.g., of 50-500 nucleotides containing the locus of the polymorphism to be analyzed. Target is usually labeled in the course of amplification. The amplification product can be RNA or DNA, single stranded or double stranded. If double stranded, the amplification product is typically denatured before application to an array. If genomic DNA is analyzed without amplification, it may be desirable to remove RNA from the sample before applying it to the array. Such can be accomplished by digestion with DNase-free RNase.

#### **DETECTION OF POLYMORPHISMS IN A NUCLEIC ACID SAMPLE**

The SNPs disclosed herein can be used to determine which forms of a characterized polymorphism are present in individuals under analysis.

The design and use of allele-specific probes for analyzing polymorphisms is described by e.g., Saiki et al., Nature 324, 163-166 (1986); Dattagupta, EP 235,726, Saiki, WO 89/11548. Allele-specific probes can be designed that hybridize to a segment of target DNA from one individual but do not hybridize to the corresponding segment from another individual due to the presence of different polymorphic forms in the respective segments from the two individuals. Hybridization conditions should be sufficiently stringent that there is a significant difference in hybridization intensity between alleles, and preferably an essentially binary response, whereby a probe hybridizes to only one of the alleles. Some probes are designed to hybridize to a segment of target DNA such that the polymorphic site aligns with a central position (e.g., in a 15-mer at the 7 position; in a 16-mer, at either the 7, 8 or 9 position) of the probe. This design of probe achieves good discrimination in hybridization between different allelic forms.

Allele-specific probes are often used in pairs, one member of a pair showing a perfect match to a reference form of a target sequence and the other member showing a perfect match to a variant form. Several pairs of probes can then be immobilized on the same support for simultaneous analysis of multiple polymorphisms within the same target sequence.

The polymorphisms can also be identified by hybridization to nucleic acid arrays, some examples of which are described in published PCT application WO 95/11995.

WO 95/11995 also describes subarrays that are optimized for detection of a variant form of a precharacterized polymorphism. Such a subarray contains probes designed to be  
5 complementary to a second reference sequence, which is an allelic variant of the first reference sequence. The second group of probes is designed by the same principles, except that the probes exhibit complementarity to the second reference sequence. The inclusion of a second group (or further groups) can be particularly useful for analyzing short subsequences of the primary reference sequence in which multiple mutations are  
10 expected to occur within a short distance commensurate with the length of the probes (e.g., two or more mutations within 9 to 21 bases).

An allele-specific primer hybridizes to a site on a target DNA overlapping a polymorphism and only primes amplification of an allelic form to which the primer exhibits perfect complementarity. See Gibbs, Nucleic Acid Res. 17 2427-2448 (1989).  
15 This primer is used in conjunction with a second primer which hybridizes at a distal site. Amplification proceeds from the two-primers, resulting in a detectable product which indicates the particular allelic form is present. A control is usually performed with a second pair of primers, one of which shows a single base mismatch at the polymorphic site and the other of which exhibits perfect complementarity to a distal site. The single-  
20 base mismatch prevents amplification and no detectable product is formed. The method works best when the mismatch is included in the 3'-most position of the oligonucleotide aligned with the polymorphism because this position is most destabilizing to elongation from the primer (see, e.g., WO 93/22456).

Amplification products generated using the polymerase chain reaction can be  
25 analyzed by the use of denaturing gradient gel electrophoresis. Different alleles can be identified based on the different sequence-dependent melting properties and electrophoretic migration of DNA in solution. Erlich, ed., PCR Technology, Principles and Applications for DNA Amplification, (W.H. Freeman and Co New York, 1992, Chapter 7).

Alleles of target sequences can be differentiated using single-strand conformation polymorphism analysis, which identifies base differences by alteration in electrophoretic migration of single stranded PCR products, as described in Orita et al., Proc. Nat. Acad. Sci. 86, 2766-2770 (1989). Amplified PCR products can be generated and heated or otherwise denatured, to form single stranded amplification products. Single-stranded nucleic acids may refold or form secondary structures which are partially dependent on the base sequence. The different electrophoretic mobilities of single-stranded amplification products can be related to base-sequence differences between alleles of target sequences.

The genotype of an individual with respect to a pathology suspected of being caused by a genetic polymorphism may be assessed by association analysis. Phenotypic traits suitable for association analysis include diseases that have known but hitherto unmapped genetic components (e.g., agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary hemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos syndrome, osteogenesis imperfecta, and acute intermittent porphyria).

Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, system, diseases of the nervous and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, oral cavity, ovary, pancreas, prostate, skin, stomach, leukemia, liver, lung, and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic treatments.

Determination of which polymorphic forms occupy a set of polymorphic sites in an individual identifies a set of polymorphic forms that distinguishes the individual. See generally National Research Council, *The Evaluation of Forensic DNA Evidence* (Eds. Pollard et al., National Academy Press, DC, 1996). Since the polymorphic sites are within a 50,000 bp region in the human genome, the probability of recombination between these polymorphic sites is low. That low probability means the haplotype (the set of all 10 polymorphic sites) set forth in this application should be inherited without change for at least several generations. The more sites that are analyzed the lower the probability that the set of polymorphic forms in one individual is the same as that in an unrelated individual. Preferably, if multiple sites are analyzed, the sites are unlinked. Thus, polymorphisms of the invention are often used in conjunction with polymorphisms in distal genes. Preferred polymorphisms for use in forensics are diallelic because the population frequencies of two polymorphic forms can usually be determined with greater accuracy than those of multiple polymorphic forms at multi-allelic loci.

The capacity to identify a distinguishing or unique set of forensic markers in an individual is useful for forensic analysis. For example, one can determine whether a blood sample from a suspect matches a blood or other tissue sample from a crime scene by determining whether the set of polymorphic forms occupying selected polymorphic sites is the same in the suspect and the sample. If the set of polymorphic markers does not match between a suspect and a sample, it can be concluded (barring experimental error) that the suspect was not the source of the sample. If the set of markers does match, one can conclude that the DNA from the suspect is consistent with that found at the crime scene. If frequencies of the polymorphic forms at the loci tested have been determined (e.g., by analysis of a suitable population of individuals), one can perform a statistical analysis to determine the probability that a match of suspect and crime scene sample would occur by chance.

$p(\text{ID})$  is the probability that two random individuals have the same polymorphic or allelic form at a given polymorphic site. In diallelic loci, four genotypes are possible: AA, AB, BA, and BB. If alleles A and B occur in a haploid genome of the organism with frequencies  $x$  and  $y$ , the probability of each genotype in a diploid organism are (see WO

95/12607):

$$\text{Homozygote: } p(AA)=x^2$$

$$\text{Homozygote: } p(BB)=y^2=(1-x)^2$$

$$\text{Single Heterozygote: } p(AB)=p(BA)=xy=x(1-x)$$

$$5 \quad \text{Both Heterozygotes: } p(AB+BA)=2xy=2x(1-x)$$

The probability of identity at one locus (i.e, the probability that two individuals, picked at random from a population will have identical polymorphic forms at a given locus) is given by the equation:

$$p(ID)=(x^2)^2+(2xy)^2+(y^2)^2.$$

- 10 These calculations can be extended for any number of polymorphic forms at a given locus. For example, the probability of identity  $p(ID)$  for a 3-allele system where the alleles have the frequencies in the population of  $x$ ,  $y$  and  $z$ , respectively, is equal to the sum of the squares of the genotype frequencies:

$$p(ID)=x^4+(2xy)^2+(2yz)^2+(2xz)^2+z^4+y^4$$

- 15 In a locus of  $n$  alleles, the appropriate binomial expansion is used to calculate  $p(ID)$  and  $p(exc)$ .

The cumulative probability of identity ( $\text{cum } p(ID)$ ) for each of multiple unlinked loci is determined by multiplying the probabilities provided by each locus:

$$\text{cum } p(ID)=p(ID1)p(ID2)p(ID3) \dots p(IDn)$$

- 20 The cumulative probability of non-identity for  $n$  loci (i.e. the probability that two random individuals will be different at 1 or more loci) is given by the equation:

$$\text{cum } p(nonID)=1-\text{cum } p(ID).$$

If several polymorphic loci are tested, the cumulative probability of non-identity for random individuals becomes very high (e.g., one billion to one). Such probabilities can be taken into account together with other evidence in determining the guilt or innocence of the suspect.

5           The object of paternity testing is usually to determine whether a male is the father of a child. In most cases, the mother of the child is known and thus, the mother's contribution to the child's genotype can be traced. Paternity testing investigates whether the part of the child's genotype not attributable to the mother is consistent with that of the putative father. Paternity testing can be performed by analyzing sets of polymorphisms in  
10   the putative father and the child.

          If the set of polymorphisms in the child attributable to the father does not match the putative father, it can be concluded, barring experimental error, that the putative father is not the real father. If the set of polymorphisms in the child attributable to the father does match the set of polymorphisms of the putative father, a statistical calculation  
15   can be performed to determine the probability of coincidental match.

          The probability of parentage exclusion (representing the probability that a random male will have a polymorphic form at a given polymorphic site that makes him incompatible as the father) is given by the equation (see WO 95/12607):

$$p(exc)=xy(1-xy)$$

20   where x and y are the population frequencies of alleles A and B of a diallelic polymorphic site. (At a triallelic site  $p(exc)=xy(1-xy)+yz(1-yz)+xz(1-xz)+3xyz(1-xyz)$ ), where x, y and z are the respective population frequencies of alleles A, B and C). The probability of non-exclusion is:

$$p(non-exc)=1-p(exc)$$

25   The cumulative probability of non-exclusion (representing the value obtained when n loci are used) is thus:

$$cum\ p(non-exc)=p(non-exc1)p(non-exc2)p(non-exc3) \dots p(non-excn)$$

The cumulative probability of exclusion for  $n$  loci (representing the probability that a random male will be excluded) is:

$$\text{cum } p(\text{exc}) = 1 - \text{cum } p(\text{non-exc}).$$

If several polymorphic loci are included in the analysis, the cumulative probability of exclusion of a random male is very high. This probability can be taken into account in assessing the liability of a putative father whose polymorphic marker set matches the child's polymorphic marker set attributable to his/her father.

The polymorphisms of the invention may contribute to the phenotype of an organism in different ways. Some polymorphisms occur within a protein coding sequence and contribute to phenotype by affecting protein structure. The effect may be neutral, beneficial or detrimental, or both beneficial and detrimental, depending on the circumstances. For example, a heterozygous sickle cell mutation confers resistance to malaria, but a homozygous sickle cell mutation is usually lethal. Other polymorphisms occur in noncoding regions but may exert phenotypic effects indirectly via influence on replication, transcription, and translation. A single polymorphism may affect more than one phenotypic trait. Likewise, a single phenotypic trait may be affected by polymorphisms in different genes. Further, some polymorphisms predispose an individual to a distinct mutation that is causally related to a certain phenotype.

Phenotypic traits include diseases that have known but hitherto unmapped genetic components. Phenotypic traits also include symptoms of, or susceptibility to, multifactorial diseases of which a component is or may be genetic, such as autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. Some examples of autoimmune diseases include rheumatoid arthritis, multiple sclerosis, diabetes (insulin-dependent and non-independent), systemic lupus erythematosus and Graves disease. Some examples of cancers include cancers of the bladder, brain, breast, colon, esophagus, kidney, leukemia, liver, lung, oral cavity, ovary, pancreas, prostate, skin, stomach and uterus. Phenotypic traits also include characteristics such as longevity, appearance (e.g., baldness, obesity), strength, speed, endurance, fertility, and susceptibility or receptivity to particular drugs or therapeutic



treatments.

Correlation is performed for a population of individuals who have been tested for the presence or absence of a phenotypic trait of interest and for polymorphic marker sets. To perform such analysis, the presence or absence of a set of polymorphisms (i.e. a polymorphic set) is determined for a set of the individuals, some of whom exhibit a particular trait, and some of whom exhibit lack of the trait. The alleles of each polymorphism of the set are then reviewed to determine whether the presence or absence of a particular allele is associated with the trait of interest. Correlation can be performed by standard statistical methods and statistically significant correlations between polymorphic form(s) and phenotypic characteristics are noted. For example, it might be found that the presence of allele A1 at polymorphism A correlates with heart disease. As a further example, it might be found that the combined presence of allele A1 at polymorphism A and allele B1 at polymorphism B correlates with increased milk production of a farm animal.

Such correlations can be exploited in several ways. In the case of a strong correlation between a set of one or more polymorphic forms and a disease for which treatment is available, detection of the polymorphic form set in a human or animal patient may justify immediate administration of treatment, or at least the institution of regular monitoring of the patient. Detection of a polymorphic form correlated with serious disease in a couple contemplating a family may also be valuable to the couple in their reproductive decisions. For example, the female partner might elect to undergo in vitro fertilization to avoid the possibility of transmitting such a polymorphism from her husband to her offspring. In the case of a weaker, but still statistically significant correlation between a polymorphic set and human disease, immediate therapeutic intervention or monitoring may not be justified. Nevertheless, the patient can be motivated to begin simple life-style changes (e.g., diet, exercise) that can be accomplished at little cost to the patient but confer potential benefits in reducing the risk of conditions to which the patient may have increased susceptibility by virtue of variant alleles. Identification of a polymorphic set in a patient correlated with enhanced receptiveness to one of several treatment regimes for a disease indicates that this

treatment regime should be followed.

For animals and plants, correlations between characteristics and phenotype are useful for breeding for desired characteristics. For example, Beitz et al., U.S. Pat. No. 5,292,639 discuss use of bovine mitochondrial polymorphisms in a breeding program to improve milk production in cows. To evaluate the effect of mtDNA D-loop sequence polymorphism on milk production, each cow was assigned a value of 1 if variant or 0 if wild type with respect to a prototypical mitochondrial DNA sequence at each of 17 locations considered.

The previous section concerns identifying correlations between phenotypic traits and polymorphisms that directly or indirectly contribute to those traits. The present section describes identification of a physical linkage between a genetic locus associated with a trait of interest and polymorphic markers that are not associated with the trait, but are in physical proximity with the genetic locus responsible for the trait and co-segregate with it. Such analysis is useful for mapping a genetic locus associated with a phenotypic trait to a chromosomal position, and thereby cloning gene(s) responsible for the trait. See Lander et al., *Proc. Natl. Acad. Sci. (USA)* 83, 7353-7357 (1986); Lander et al., *Proc. Natl. Acad. Sci. (USA)* 84, 2363-2367 (1987); Donis-Keller et al., *Cell* 51, 319-337 (1987); Lander et al., *Genetics* 121, 185-199 (1989)). Genes localized by linkage can be cloned by a process known as directional cloning. See Wainwright, *Med. J. Australia* 159, 170-174 (1993); Collins, *Nature Genetics* 1, 3-6 (1992) (each of which is incorporated by reference in its entirety for all purposes).

Linkage studies are typically performed on members of a family. Available members of the family are characterized for the presence or absence of a phenotypic trait and for a set of polymorphic markers. The distribution of polymorphic markers in an informative meiosis is then analyzed to determine which polymorphic markers co-segregate with a phenotypic trait. See, e.g., Kerem et al., *Science* 245, 1073-1080 (1989); Monaco et al., *Nature* 316, 842 (1985); Yamoka et al., *Neurology* 40, 222-226 (1990); Rossiter et al., *FASEB Journal* 5, 21-27 (1991).

Linkage is analyzed by calculation of LOD (log of the odds) values. A lod value

is the relative likelihood of obtaining observed segregation data for a marker and a genetic locus when the two are located at a recombination fraction  $RF$ , versus the situation in which the two are not linked, and thus segregating independently (Thompson & Thompson, *Genetics in Medicine* (5th ed, W.B. Saunders Company, Philadelphia, 1991); Strachan, "Mapping the human genome" in *The Human Genome* (BIOS Scientific Publishers Ltd, Oxford), Chapter 4). A series of likelihood ratios are calculated at various recombination fractions ( $RF$ ), ranging from  $RF=0.0$  (coincident loci) to  $RF=0.50$  (unlinked). Thus, the likelihood at a given value of  $RF$  is: probability of data if loci linked at  $RF$  to probability of data if loci unlinked. The computed likelihood is usually expressed as the  $\log_{10}$  of this ratio (i.e., a lod score). For example, a lod score of 3 indicates 1000:1 odds against an apparent observed linkage being a coincidence. The use of logarithms allows data collected from different families to be combined by simple addition. Computer programs are available for the calculation of lod scores for differing values of  $RF$  (e.g., LIPED, MLINK (Lathrop, *Proc. Nat. Acad. Sci. (USA)* 81, 3443-3446 (1984)). For any particular lod score, a recombination fraction may be determined from mathematical tables. See Smith et al., *Mathematical tables for research workers in human genetics* (Churchill, London, 1961); Smith, *Ann. Hum. Genet.* 32, 127-150 (1968). The value of  $RF$  at which the lod score is the highest is considered to be the best estimate of the recombination fraction.

Positive lod score values suggest that the two loci are linked, whereas negative values suggest that linkage is less likely (at that value of  $RF$ ) than the possibility that the two loci are unlinked. By convention, a combined lod score of + 3 or greater (equivalent to greater than 1000:1 odds in favor of linkage) is considered definitive evidence that two loci are linked. Similarly, by convention, a negative lod score of -2 or less is taken as definitive evidence against linkage of the two loci being compared. Negative linkage data are useful in excluding a chromosome or a segment thereof from consideration. The search focuses on the remaining non-excluded chromosomal locations.

The invention further provides transgenic nonhuman animals capable of expressing an exogenous variant gene and/or having one or both alleles of an endogenous variant gene inactivated. Expression of an exogenous variant gene is usually achieved

by operably linking the gene to a promoter and optionally an enhancer, and microinjecting the construct into a zygote. See Hogan et al., "Manipulating the Mouse Embryo, A Laboratory Manual," Cold Spring Harbor Laboratory. (1989). Inactivation of endogenous variant genes can be achieved by forming a transgene in which a cloned variant gene is inactivated by insertion of a positive selection marker. See Capecchi, Science 244, 1288-1292 The transgene is then introduced into an embryonic stem cell, where it undergoes homologous recombination with an endogenous variant gene. Mice and other rodents are preferred animals. Such animals provide useful drug screening systems.

The invention further provides methods for assessing the pharmacogenomic susceptibility of a subject harboring a single nucleotide polymorphism to a particular pharmaceutical compound, or to a class of such compounds. Genetic polymorphism in drug-metabolizing enzymes, drug transporters, receptors for pharmaceutical agents, and other drug targets have been correlated with individual differences based on distinction in the efficacy and toxicity of the pharmaceutical agent administered to a subject. Pharmacogenomic characterization of a subjects susceptibility to a drug enhances the ability to tailor a dosing regimen to the particular genetic constitution of the subject, thereby enhancing and optimizing the therapeutic effectiveness of the therapy.

In cases in which a cSNP leads to a polymorphic protein that is ascribed to be the cause of a pathological condition, method of treating such a condition includes administering to a subject experiencing the pathology the wild type cognate of the polymorphic protein. Once administered in an effective dosing regimen, the wild type cognate provides complementation or remediation of the defect due to the polymorphic protein. The subject's condition is ameliorated by this protein therapy.

A subject suspected of suffering from a pathology ascribable to a polymorphic protein that arises from a cSNP is to be diagnosed using any of a variety of diagnostic methods capable of identifying the presence of the cSNP in the nucleic acid, or of the cognate polymorphic protein, in a suitable clinical sample taken from the subject. Once the presence of the cSNP has been ascertained, and the pathology is correctable by

administering a normal or wild-type gene, the subject is treated with a pharmaceutical composition that includes a nucleic acid that harbors the correcting wild-type gene, or a fragment containing a correcting sequence of the wild-type gene. Non-limiting examples of ways in which such a nucleic acid may be administered include incorporating the wild-type gene in a viral vector, such as an adenovirus or adeno associated virus, and administration of a naked DNA in a pharmaceutical composition that promotes intracellular uptake of the administered nucleic acid. Once the nucleic acid that includes the gene coding for the wild-type allele of the polymorphism is incorporated within a cell of the subject, it will initiate *de novo* biosynthesis of the wild-type gene product. If the nucleic acid is further incorporated into the genome of the subject, the treatment will have long-term effects, providing *de novo* synthesis of the wild-type protein for a prolonged duration. The synthesis of the wild-type protein in the cells of the subject will contribute to a therapeutic enhancement of the clinical condition of the subject.

A subject suffering from a pathology ascribed to a SNP may be treated so as to correct the genetic defect. (See Kren et al., Proc. Natl. Acad. Sci. USA 96:10349-10354 (1999)). Such a subject is identified by any method that can detect the polymorphism in a sample drawn from the subject. Such a genetic defect may be permanently corrected by administering to such a subject a nucleic acid fragment incorporating a repair sequence that supplies the wild-type nucleotide at the position of the SNP. This site-specific repair sequence encompasses an RNA/DNA oligonucleotide which operates to promote endogenous repair of a subject's genomic DNA. Upon administration in an appropriate vehicle, such as a complex with polyethylenimine or encapsulated in anionic liposomes, a genetic defect leading to an inborn pathology may be overcome, as the chimeric oligonucleotides induces incorporation of the wild-type sequence into the subject's genome. Upon incorporation, the wild-type gene product is expressed, and the replacement is propagated, thereby engendering a permanent repair.

The invention further provides kits comprising at least one allele-specific oligonucleotide as described above. Often, the kits contain one or more pairs of allele-specific oligonucleotides hybridizing to different forms of a polymorphism. In some kits, the allele-specific oligonucleotides are provided immobilized to a substrate. For

example, the same substrate can comprise allele-specific oligonucleotide probes for detecting at least 10, 100, 1000 or all of the polymorphisms shown in the Table. Optional additional components of the kit include, for example, restriction enzymes, reverse-transcriptase or polymerase, the substrate nucleoside triphosphates, means used to label (for example, an avidin-enzyme conjugate and enzyme substrate and chromogen if the label is biotin), and the appropriate buffers for reverse transcription, PCR, or hybridization reactions. Usually, the kit also contains instructions for carrying out the hybridizing methods.

Several aspects of the present invention rely on having available the polymorphic proteins encoded by the nucleic acids comprising a SNP of the inventions. There are various methods of isolating these nucleic acid sequences. For example, DNA is isolated from a genomic or cDNA library using labeled oligonucleotide probes having sequences complementary to the sequences disclosed herein.

Such probes can be used directly in hybridization assays. Alternatively probes can be designed for use in amplification techniques such as PCR.

To prepare a cDNA library, mRNA is isolated from tissue such as heart or pancreas, preferably a tissue wherein expression of the gene or gene family is likely to occur. cDNA is prepared from the mRNA and ligated into a recombinant vector. The vector is transfected into a recombinant host for propagation, screening and cloning. Methods for making and screening cDNA libraries are well known, See Gubler, U. and Hoffman, B.J. *Gene* 25:263-269 (1983) and Sambrook et al.

For a genomic library, for example, the DNA is extracted from tissue and either mechanically sheared or enzymatically digested to yield fragments of about 12-20 kb. The fragments are then separated by gradient centrifugation from undesired sizes and are constructed in bacteriophage lambda vectors. These vectors and phage are packaged *in vitro*, as described in Sambrook, et al. Recombinant phage are analyzed by plaque hybridization as described in Benton and Davis, *Science* 196:180-182 (1977). Colony hybridization is carried out as generally described in M. Grunstein et al. *Proc. Natl. Acad. Sci. USA*. 72:3961-3965 (1975). DNA of interest is identified in either cDNA or

genomic libraries by its ability to hybridize with nucleic acid probes, for example on Southern blots, and these DNA regions are isolated by standard methods familiar to those of skill in the art. See Sambrook, et al.

In PCR techniques, oligonucleotide primers complementary to the two 3' borders of the DNA region to be amplified are synthesized. The polymerase chain reaction is then carried out using the two primers. See PCR Protocols: a Guide to Methods and Applications (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Primers can be selected to amplify the entire regions encoding a full-length sequence of interest or to amplify smaller DNA segments as desired. PCR can be used in a variety of protocols to isolate cDNAs encoding a sequence of interest. In these protocols, appropriate primers and probes for amplifying DNA encoding a sequence of interest are generated from analysis of the DNA sequences listed herein. Once such regions are PCR-amplified, they can be sequenced and oligonucleotide probes can be prepared from the sequence.

Once DNA encoding a sequence comprising a cSNP is isolated and cloned, one can express the encoded polymorphic proteins in a variety of recombinantly engineered cells. It is expected that those of skill in the art are knowledgeable in the numerous expression systems available for expression of DNA encoding a sequence of interest. No attempt to describe in detail the various methods known for the expression of proteins in prokaryotes or eukaryotes is made here.

In brief summary, the expression of natural or synthetic nucleic acids encoding a sequence of interest will typically be achieved by operably linking the DNA or cDNA to a promoter (which is either constitutive or inducible), followed by incorporation into an expression vector. The vectors can be suitable for replication and integration in either prokaryotes or eukaryotes. Typical expression vectors contain initiation sequences, transcription and translation terminators, and promoters useful for regulation of the expression of a polynucleotide sequence of interest. To obtain high level expression of a cloned gene, it is desirable to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for

translational initiation, and a transcription/translation terminator. The expression vectors may also comprise generic expression cassettes containing at least one independent terminator sequence, sequences permitting replication of the plasmid in both eukaryotes and prokaryotes, i.e., shuttle vectors, and selection markers for both prokaryotic and eukaryotic systems. See Sambrook et al.

A variety of prokaryotic expression systems may be used to express the polymorphic proteins of the invention. Examples include *E. coli*, *Bacillus*, *Streptomyces*, and the like.

It is preferred to construct expression plasmids which contain, at the minimum, a strong promoter to direct transcription, a ribosome binding site for translational initiation, and a transcription/translation terminator. Examples of regulatory regions suitable for this purpose in *E. coli* are the promoter and operator region of the *E. coli* tryptophan biosynthetic pathway as described by Yanofsky, C., J. Bacterial. 158:1018-1024 (1984) and the leftward promoter of phage lambda as described by Λ, I. and Hagen, D., Ann. Rev. Genet. 14:399-445 (1980). The inclusion of selection markers in DNA vectors transformed in *E. coli* is also useful. Examples of such markers include genes specifying resistance to ampicillin, tetracycline, or chloramphenicol. See Sambrook et al. for details concerning selection markers for use in *E. coli*.

To enhance proper folding of the expressed recombinant protein, during purification from *E. coli*, the expressed protein may first be denatured and then renatured. This can be accomplished by solubilizing the bacterially produced proteins in a chaotropic agent such as guanidine HCl and reducing all the cysteine residues with a reducing agent such as beta-mercaptoethanol. The protein is then renatured, either by slow dialysis or by gel filtration. See U.S. Patent No. 4,511,503. Detection of the expressed antigen is achieved by methods known in the art as radioimmunoassay, or Western blotting techniques or immunoprecipitation. Purification from *E. coli* can be achieved following procedures such as those described in U.S. Patent No. 4,511,503.

Any of a variety of eukaryotic expression systems such as yeast, insect cell lines, bird, fish, and mammalian cells, may also be used to express a polymorphic protein of the



invention. As explained briefly below, a nucleotide sequence harboring a cSNP may be expressed in these eukaryotic systems. Synthesis of heterologous proteins in yeast is well known. Methods in Yeast Genetics, Sherman, F., et al., Cold Spring Harbor Laboratory, (1982) is a well recognized work describing the various methods available to produce the protein in yeast. Suitable vectors usually have expression control sequences, such as promoters, including 3-phosphoglycerate kinase or other glycolytic enzymes, and an origin of replication, termination sequences and the like as desired. For instance, suitable vectors are described in the literature (Botstein, et al., *Gene* 8:17-24 (1979); Broach, et al., *Gene* 8:121-133 (1979)).

Two procedures are used in transforming yeast cells. In one case, yeast cells are first converted into protoplasts using zymolyase, lyticase or glucanase, followed by addition of DNA and polyethylene glycol (PEG). The PEG-treated protoplasts are then regenerated in a 3% agar medium under selective conditions. Details of this procedure are given in the papers by J.D. Beggs, *Nature* (London) 275:104-109 (1978); and Hinnen, A., et al., *Proc. Natl. Acad. Sci. USA*, 75:1929-1933 (1978). The second procedure does not involve removal of the cell wall. Instead the cells are treated with lithium chloride or acetate and PEG and put on selective plates (Ito, H., et al., *J. Bact.* 153:163-168 (1983)) cells and applying standard protein isolation techniques to the lysates.

The purification process can be monitored by using Western blot techniques or radioimmunoassay or other standard techniques. The sequences encoding the proteins of the invention can also be ligated to various immunoassay expression vectors for use in transforming cell cultures of, for instance, mammalian, insect, bird or fish origin. Illustrative of cell cultures useful for the production of the polypeptides are mammalian cells. Mammalian cell systems often will be in the form of monolayers of cells although mammalian cell suspensions may also be used. A number of suitable host cell lines capable of expressing intact proteins have been developed in the art, and include the HEK293, BHK21, and CHO cell lines, and various human cells such as COS cell lines, HeLa cells, myeloma cell lines, Jurkat cells, etc. Expression vectors for these cells can include expression control sequences, such as an origin of replication, a promoter (e.g.,

the CMV promoter, a HSV *tk* promoter or *pgk* (phosphoglycerate kinase) promoter), an enhancer (Queen et al. Immunol. Rev. 89:49 (1986)) and necessary processing information sites, such as ribosome binding sites, RNA splice sites, polyadenylation sites (e.g., an SV40 large T Ag poly A addition site), and transcriptional terminator sequences.

5 Other animal cells are available, for instance, from the American Type Culture Collection Catalogue of Cell Lines and Hybridomas (7th edition, (1992)). Appropriate vectors for expressing the proteins of the invention in insect cells are usually derived from baculovirus. Insect cell lines include mosquito larvae, silkworm, armyworm, moth and *Drosophila* cell lines such as a Schneider cell line (See Schneider J. Embryol. Exp. Morphol., 27:353-365 (1987). As indicated above, the vector, e.g., a plasmid, which is used to transform the host cell, preferably contains DNA sequences to initiate transcription and sequences to control the translation of the protein. These sequences are referred to as expression control sequences. As with yeast, when higher animal host cells are employed, polyadenylation or transcription terminator sequences from known

10 mammalian genes need to be incorporated into the vector. An example of a terminator sequence is the polyadenylation sequence from the bovine growth hormone gene. Sequences for accurate splicing of the transcript may also be included. An example of a splicing sequence is the VP1 intron from SV40 (Sprague, J. et al., J. Virol. 45: 773-781 (1983)). Additionally, gene sequences to control replication in the host cell may be

15 Saveria-Campo, M., 1985, "Bovine Papilloma virus DNA a Eukaryotic Cloning Vector" in DNA Cloning Vol. II a Practical Approach Ed. D.M. Glover, IRL Press, Arlington, Virginia pp. 213-238. The host cells are competent or rendered competent for transformation by various means. There are several well-known methods of introducing DNA into animal cells. These include: calcium phosphate precipitation, fusion of the

20 recipient cells with bacterial protoplasts containing the DNA, treatment of the recipient cells with liposomes containing the DNA, DEAE dextran, electroporation and micro-injection of the DNA directly into the cells.

The transformed cells are cultured by means well known in the art (Biochemical Methods in Cell Culture and Virology, Kuchler, R.J., Dowden, Hutchinson and Ross, Inc., (1977)). The expressed polypeptides are isolated from cells grown as suspensions or

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as monolayers. The latter are recovered by well known mechanical, chemical or enzymatic means.

General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, Methods in Enzymology 185, 537-566 (1990). As defined herein “operably linked” refers to linkage of a promoter upstream from a DNA sequence such that the promoter mediates transcription of the DNA sequence. Specifically, “operably linked” means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the gene encoding the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression sequence. The term “vector”, refers to viral expression systems, autonomous self-replicating circular DNA (plasmids), and includes both expression and nonexpression plasmids.

The term “gene” as used herein is intended to refer to a nucleic acid sequence which encodes a polypeptide. This definition includes various sequence polymorphisms, mutations, and/or sequence variants wherein such alterations do not affect the function of the gene product. The term “gene” is intended to include not only coding sequences but also regulatory regions such as promoters, enhancers, termination regions and similar untranslated nucleotide sequences. The term further includes all introns and other DNA sequences spliced from the mRNA transcript, along with variants resulting from alternative splice sites.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A43 1 cells, human Co10205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from in vitro culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL- 60, U937, HaK or Jurkat cells. Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains,

Candida or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, e.g., Invitrogen, San Diego, California, U.S.A. (the MaxBac© kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed." The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein.

The polymorphic protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein. The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art.

The polymorphic proteins produced by recombinant DNA technology may be purified by techniques commonly employed to isolate or purify recombinant proteins. Recombinantly produced proteins can be directly expressed or expressed as a fusion protein. The protein is then purified by a combination of cell lysis (e.g., sonication) and affinity chromatography. For fusion products, subsequent digestion of the fusion protein with an appropriate proteolytic enzyme releases the desired polypeptide. The polypeptides of this invention may be purified to substantial purity by standard

techniques well known in the art, including selective precipitation with such substances as ammonium sulfate, column chromatography, immunopurification methods, and others. See, for instance, R. Scopes, Protein Purification: Principles and Practice, Springer-Verlag: New York (1982), incorporated herein by reference. For example, in an  
5 embodiment, antibodies may be raised to the proteins of the invention as described herein. Cell membranes are isolated from a cell line expressing the recombinant protein, the protein is extracted from the membranes and immunoprecipitated. The proteins may then be further purified by standard protein chemistry techniques as described above.

The resulting expressed protein may then be purified from such culture (i.e.,  
10 from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-Toyopearl@ or Cibacrom blue 3GA Sepharose B; one or more steps involving hydrophobic interaction  
15 chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography. Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such  
20 fusion proteins are commercially available from New England BioLab (Beverly, MA), Pharmacia (Piscataway, NJ) and InVitrogen, respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from Kodak (New Haven, CT). Finally, one or more reverse-phase high performance liquid chromatography (RP-  
25 HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance  
30 with the present invention as an "isolated protein."

The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as polymorphic. Such antibodies include, but are not limited to, polyclonal,  
5 monoclonal, chimeric, single chain,  $F_{ab}$  and  $F_{(ab)2}$  fragments, and an  $F_{ab}$  expression library. In a specific embodiment, antibodies to human polymorphic proteins are disclosed.

The phrase "specifically binds to", "immunospecifically binds to" or is "specifically immunoreactive with", an antibody when referring to a protein or peptide,  
10 refers to a binding reaction which is determinative of the presence of the protein in the presence of a heterogeneous population of proteins and other biological materials. Thus, for example, under designated immunoassay conditions, the specified antibodies bind to a particular protein and do not bind in a significant amount to other proteins present in the sample. Specific binding to an antibody under such conditions may require an antibody  
15 that is selected for its specificity for a particular protein. Of particular interest in the present invention is an antibody that binds immunospecifically to a polymorphic protein but not to its cognate wild type allelic protein, or vice versa. A variety of immunoassay formats may be used to select antibodies specifically immunoreactive with a particular protein. For example, solid-phase ELISA immunoassays are routinely used to select  
20 monoclonal antibodies specifically immunoreactive with a protein. See Harlow and Lane (1988) Antibodies, a Laboratory Manual, Cold Spring Harbor Publications, New York, for a description of immunoassay formats and conditions that can be used to determine specific immunoreactivity.

Polyclonal and/or monoclonal antibodies that immunospecifically bind to  
25 polymorphic gene products but not to the corresponding prototypical or "wild-type" gene products are also provided. Antibodies can be made by injecting mice or other animals with the variant gene product or synthetic peptide. Monoclonal antibodies are screened as are described, for example, in Harlow & Lane, Antibodies, A Laboratory Manual, Cold Spring Harbor Press, New York (1988); Goding, Monoclonal antibodies, Principles  
30 and Practice (2d ed.) Academic Press, New York (1986). Monoclonal antibodies are

tested for specific immunoreactivity with a variant gene product and lack of immunoreactivity to the corresponding prototypical gene product.

An isolated polymorphic protein, or a portion or fragment thereof, can be used as an immunogen to generate the antibody that binds the polymorphic protein using standard techniques for polyclonal and monoclonal antibody preparation. The full-length polymorphic protein can be used or, alternatively, the invention provides antigenic peptide fragments of polymorphic for use as immunogens. The antigenic peptide of a polymorphic protein of the invention comprises at least 8 amino acid residues of the amino acid sequence encompassing the polymorphic amino acid and encompasses an epitope of the polymorphic protein such that an antibody raised against the peptide forms a specific immune complex with the polymorphic protein. Preferably, the antigenic peptide comprises at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues. Preferred epitopes encompassed by the antigenic peptide are regions of polymorphic that are located on the surface of the protein, *e.g.*, hydrophilic regions.

For the production of polyclonal antibodies, various suitable host animals (*e.g.*, rabbit, goat, mouse or other mammal) may be immunized by injection with the polymorphic protein. An appropriate immunogenic preparation can contain, for example, recombinantly expressed polymorphic protein or a chemically synthesized polymorphic polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (*e.g.*, aluminum hydroxide), surface active substances (*e.g.*, lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against polymorphic proteins can be isolated from the mammal (*e.g.*, from the blood) and further purified by well known techniques, such as protein A chromatography, to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that originates from the clone of a singly hybridoma cell, and that contains only one type of antigen binding site capable of immunoreacting with a particular epitope of a polymorphic protein. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polymorphic protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular polymorphic protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96).

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a polymorphic protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methodologies can be adapted for the construction of  $F_{ab}$  expression libraries (see *e.g.*, Huse, *et al.*, 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal  $F_{ab}$  fragments with the desired specificity for a polymorphic protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Antibody fragments that contain the idiotypes to a polymorphic protein may be produced by techniques known in the art including, but not limited to: (i) an  $F_{(ab)2}$  fragment produced by pepsin digestion of an antibody molecule; (ii) an  $F_{ab}$  fragment generated by reducing the disulfide bridges of an  $F_{(ab)2}$  fragment; (iii) an  $F_{ab}$  fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv)  $F_v$  fragments.



Additionally, recombinant anti-polymorphic protein antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988) *J Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525; Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060.

In one embodiment, methodologies for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art.

Anti-polymorphic protein antibodies may be used in methods known within the art relating to the detection, quantitation and/or cellular or tissue localization of a polymorphic protein (*e.g.*, for use in measuring levels of the polymorphic protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for polymorphic proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody-derived CDR, are utilized as pharmacologically-active compounds in therapeutic applications intended to treat a pathology in a subject that arises from the presence of the cSNP allele in the subject.

An anti-polymorphic protein antibody (*e.g.*, monoclonal antibody) can be used to isolate polymorphic proteins by a variety of immunochemical techniques, such as

immunoaffinity chromatography or immunoprecipitation. An anti-polymorphic protein antibody can facilitate the purification of natural polymorphic protein from cells and of recombinantly produced polymorphic proteins expressed in host cells. Moreover, an anti-polymorphic protein antibody can be used to detect polymorphic protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the polymorphic protein. Anti-polymorphic antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance.

Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^3\text{H}$ .

## EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that unique compositions and methods of use thereof in SNPs in known genes have been described. Although particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims which follow. In particular, it is contemplated by the inventor that various substitutions, alterations, and modifications may be made to the invention without departing from the spirit and scope of the invention as defined by the claims.

**WHAT IS CLAIMED IS:**

1. An isolated polynucleotide selected from the group consisting of:
  - a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468;
  - 5 b) a fragment of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
  - c) a complementary nucleotide sequence comprising a sequence complementary to one or more of said polymorphic sequences selected from the group consisting of SEQ ID NOS:1-1468; and
  - 10 d) a fragment of said complementary nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.
2. The polynucleotide of claim 1, wherein said polynucleotide sequence is DNA.
- 15 3. The polynucleotide of claim 1, wherein said polynucleotide sequence is RNA.
4. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 100 nucleotides in length.
- 20 5. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 90 nucleotides in length.
6. The polynucleotide of claim 1, wherein said polynucleotide sequence is between about 10 and about 75 nucleotides in length.
- 25 7. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and about 50 bases in length.
8. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and about 40 bases in length.
- 30

9. The polynucleotide of claim 1, wherein said polynucleotide is between about 15 and about 30 bases in length.
10. The polynucleotide of claim 1, wherein said polymorphic site includes a nucleotide other than the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
11. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of said polymorphic sequence.
12. The polynucleotide of claim 1, wherein said polymorphic site includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
13. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes the complement of the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
14. An isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is selected from the group consisting of:
- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468 provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence;
  - b) a nucleotide sequence that is a fragment of said polymorphic sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
  - c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468, provided that the

complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and  
d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

15. The oligonucleotide of claim 14, wherein the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide selected from the group consisting of:

- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468, wherein said polymorphic sequence includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence;
- b) a nucleotide sequence that is a fragment of any of said nucleotide sequences;
- c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468, wherein said polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and
- d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

16. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 51 bases in length.

17. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 40 bases in length.

18. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 15 and about 30 bases in length.

19. A method of detecting a polymorphic site in a nucleic acid, the method comprising:

- a) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
- b) determining whether said nucleic acid and said oligonucleotide hybridize;

whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphic site in said nucleic acid.

20. The method of claim 19, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

21. The method of claim 19, wherein said oligonucleotide is between about 10 and about 51 bases in length.

22. The method of claim 19, wherein said oligonucleotide is between about 10 and about 40 bases in length.

23. A method of detecting the presence of a sequence polymorphism in a subject, the method comprising:

- a) providing a nucleic acid from said subject;
- b) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and
- c) determining whether said nucleic acid and said oligonucleotide hybridize;

whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphism in said subject.

24. A method of determining the relatedness of a first and second nucleic acid, the method comprising:

- a) providing a first nucleic acid and a second nucleic acid;
- b) contacting said first nucleic acid and said second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;
- c) determining whether said first nucleic acid and said second nucleic acid hybridize to said oligonucleotide; and
- d) comparing hybridization of said first and second nucleic acids to said oligonucleotide, wherein hybridization of first and second nucleic acids to said nucleic acid indicates the first and second subjects are related.

25. The method of claim 24, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide

recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

- 5     26.     The method of claim 24, wherein the oligonucleotide is between about 10 and about 51 bases in length.
27.     The method of claim 24, wherein the oligonucleotide is between about 10 and about 40 bases in length.
- 10     28.     The method of claim 24, wherein the oligonucleotide is between about 15 and about 30 bases in length.
- 15     29.     An isolated polypeptide comprising a polymorphic site at one or more amino acid residues, wherein the protein is encoded by a polynucleotide selected from the group consisting of polymorphic sequences SEQ ID NOS:1-1468, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the
- 20     nucleotide recited in Table 1, column 5.
- 25     30.     The polypeptide of claim 29, wherein said polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.
- 30     31.     The polypeptide of claim 29, wherein the polypeptide encoded by said polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.



32. An antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1-1468, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

33. The antibody of claim 32, wherein said antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

34. The antibody of claim 32, wherein said antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

35. A method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject, the method comprising

- a) providing a protein sample from said subject;
- b) contacting said sample with the antibody of claim 34 under conditions that allow for the formation of antibody-antigen complexes; and
- c) detecting said antibody-antigen complexes,

whereby the presence of said complexes indicates the presence of said polypeptide.

36. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

- a) providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence

selected from the group consisting of SEQ ID NOS:1 - 1468, or its complement; and

- b) administering to the subject an effective therapeutic dose of a second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele,

thereby treating said subject.

37. The method of claim 36, wherein the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

38. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

- a) providing a subject suffering from a pathology associated with aberrant expression of a polymorphic sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1 - 1468, or its complement; and

- b) administering to the subject an effective therapeutic dose of a polypeptide,

wherein said polypeptide is encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

39. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

- a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or its complement; and

- b) administering to the subject an effective dose of the antibody of claim 34,

thereby treating said subject.

40. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

- a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or its complement; and

- b) administering to the subject an effective dose of an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 1468, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 1468, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for said polymorphic sequence,

thereby treating said subject.

41. An oligonucleotide array, comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is chosen from the group consisting of:

- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468;

b) a nucleotide sequence that is a fragment of any of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;

c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 1468; and

d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

42. The array of claim 41, wherein said array comprises about 10 oligonucleotides.

43. The array of claim 41, wherein said array comprises about 100 oligonucleotides.

44. The array of claim 41, wherein said array comprises about 1000 oligonucleotides.

# ABSTRACT

The invention provides nucleic acids containing single-nucleotide polymorphisms  
5 identified for transcribed human sequences, as well as methods of using the nucleic acids.

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| Year | Age     | Sex    | Occupation | Education   | Income   | Health | Family | Community | Environment | Policy | Program | Impact | Outcome | Conclusion |
|------|---------|--------|------------|-------------|----------|--------|--------|-----------|-------------|--------|---------|--------|---------|------------|
| 1990 | 18-24   | Male   | Student    | High School | \$10,000 | Good   | 2      | 1         | 1           | 1      | 1       | 1      | 1       | 1          |
| 1991 | 25-34   | Female | Teacher    | College     | \$15,000 | Good   | 3      | 2         | 2           | 2      | 2       | 2      | 2       | 2          |
| 1992 | 35-44   | Male   | Engineer   | University  | \$20,000 | Good   | 4      | 3         | 3           | 3      | 3       | 3      | 3       | 3          |
| 1993 | 45-54   | Female | Nurse      | College     | \$18,000 | Good   | 5      | 4         | 4           | 4      | 4       | 4      | 4       | 4          |
| 1994 | 55-64   | Male   | Manager    | University  | \$25,000 | Good   | 6      | 5         | 5           | 5      | 5       | 5      | 5       | 5          |
| 1995 | 65-74   | Female | Retired    | High School | \$12,000 | Good   | 7      | 6         | 6           | 6      | 6       | 6      | 6       | 6          |
| 1996 | 75-84   | Male   | Farmer     | College     | \$14,000 | Good   | 8      | 7         | 7           | 7      | 7       | 7      | 7       | 7          |
| 1997 | 85-94   | Female | Homemaker  | High School | \$8,000  | Good   | 9      | 8         | 8           | 8      | 8       | 8      | 8       | 8          |
| 1998 | 95-104  | Male   | Unemployed | High School | \$5,000  | Good   | 10     | 9         | 9           | 9      | 9       | 9      | 9       | 9          |
| 1999 | 105-114 | Female | Unemployed | High School | \$3,000  | Good   | 11     | 10        | 10          | 10     | 10      | 10     | 10      | 10         |
| 2000 | 115-124 | Male   | Unemployed | High School | \$2,000  | Good   | 12     | 11        | 11          | 11     | 11      | 11     | 11      | 11         |
| 2001 | 125-134 | Female | Unemployed | High School | \$1,000  | Good   | 13     | 12        | 12          | 12     | 12      | 12     | 12      | 12         |
| 2002 | 135-144 | Male   | Unemployed | High School | \$500    | Good   | 14     | 13        | 13          | 13     | 13      | 13     | 13      | 13         |
| 2003 | 145-154 | Female | Unemployed | High School | \$250    | Good   | 15     | 14        | 14          | 14     | 14      | 14     | 14      | 14         |
| 2004 | 155-164 | Male   | Unemployed | High School | \$125    | Good   | 16     | 15        | 15          | 15     | 15      | 15     | 15      | 15         |
| 2005 | 165-174 | Female | Unemployed | High School | \$62     | Good   | 17     | 16        | 16          | 16     | 16      | 16     | 16      | 16         |
| 2006 | 175-184 | Male   | Unemployed | High School | \$31     | Good   | 18     | 17        | 17          | 17     | 17      | 17     | 17      | 17         |
| 2007 | 185-194 | Female | Unemployed | High School | \$15     | Good   | 19     | 18        | 18          | 18     | 18      | 18     | 18      | 18         |
| 2008 | 195-204 | Male   | Unemployed | High School | \$7      | Good   | 20     | 19        | 19          | 19     | 19      | 19     | 19      | 19         |
| 2009 | 205-214 | Female | Unemployed | High School | \$3      | Good   | 21     | 20        | 20          | 20     | 20      | 20     | 20      | 20         |
| 2010 | 215-224 | Male   | Unemployed | High School | \$1      | Good   | 22     | 21        | 21          | 21     | 21      | 21     | 21      | 21         |
| 2011 | 225-234 | Female | Unemployed | High School | \$0      | Good   | 23     | 22        | 22          | 22     | 22      | 22     | 22      | 22         |
| 2012 | 235-244 | Male   | Unemployed | High School | \$0      | Good   | 24     | 23        | 23          | 23     | 23      | 23     | 23      | 23         |
| 2013 | 245-254 | Female | Unemployed | High School | \$0      | Good   | 25     | 24        | 24          | 24     | 24      | 24     | 24      | 24         |
| 2014 | 255-264 | Male   | Unemployed | High School | \$0      | Good   | 26     | 25        | 25          | 25     | 25      | 25     | 25      | 25         |
| 2015 | 265-274 | Female | Unemployed | High School | \$0      | Good   | 27     | 26        | 26          | 26     | 26      | 26     | 26      | 26         |
| 2016 | 275-284 | Male   | Unemployed | High School | \$0      | Good   | 28     | 27        | 27          | 27     | 27      | 27     | 27      | 27         |
| 2017 | 285-294 | Female | Unemployed | High School | \$0      | Good   | 29     | 28        | 28          | 28     | 28      | 28     | 28      | 28         |
| 2018 | 295-304 | Male   | Unemployed | High School | \$0      | Good   | 30     | 29        | 29          | 29     | 29      | 29     | 29      | 29         |
| 2019 | 305-314 | Female | Unemployed | High School | \$0      | Good   | 31     | 30        | 30          | 30     | 30      | 30     | 30      | 30         |
| 2020 | 315-324 | Male   | Unemployed | High School | \$0      | Good   | 32     |           |             |        |         |        |         |            |

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|    |            |      |  |   |     |  |  |                      |                  |   |          |                 |
|----|------------|------|--|---|-----|--|--|----------------------|------------------|---|----------|-----------------|
| 7  | cg43988460 | 4708 | TACCAAAAAAAAA<br>AAAGGAAAGGA<br>AA[G]AAAGGG<br>GTGGCCTGACA<br>CTGGTGCC     | G | A   |  |  | SILENT-<br>NONCODING | cadherin         | Human Gene SWISSPROT-<br>ID:P19022 NEURAL-CADHERIN<br>PRECURSOR (N-CADHERIN) -<br>HOMO SAPIENS (HUMAN), 906 aa.   | 0.00E+00 | 18<br>(18q11.2) |
| 8  | cg43982945 | 460  | GACACATGTCA<br>GGCTGGGCGAG<br>CAG[C]gap[CACT<br>CTGATCAGCAC<br>CAGGTCCCGA  | C | gap |  |  | SILENT-<br>NONCODING | cathepsin        | Human Gene Similar to SWISSPROT-<br>ID:Q26534 CATHEPSIN L<br>PRECURSOR (EC 3.4.22.15)<br>(SMCL1) - SCHISTOSOMA<br>MANSONI (BLOOD FLUKE), 319 aa.  | 2.00E-80 | 11              |
| 9  | cg43266931 | 96   | GGGCGCTAGCG<br>GGGGTGACCGG<br>CGG[G]gap[CCG<br>GTAGGCCGCCA<br>GGATCTCGGCG  | G | gap |  |  | SILENT-<br>NONCODING | chloride channel | Human Gene Similar to SWISSNEW-<br>ID:O15247 CHLORIDE<br>INTRACELLULAR CHANNEL<br>PROTEIN 2 (XAP121) - HOMO<br>SAPIENS (HUMAN), 243<br>aa.   pds:SWISSPROT-ID:O15247<br>CHLORIDE INTRACELLULAR<br>CHANNEL PROTEIN 2 (XAP121) -<br>HOMO SAPIENS (HUMAN), 243 aa. | 3.10E-59 | 9               |
| 10 | cg43321451 | 1126 | GAAGGCACACA<br>CACACACACAC<br>ACA[C]gap[JAGCA<br>AAAGCTAAATCA<br>TCACCCGCG | C | gap |  |  | SILENT-<br>NONCODING | collagen         | Human Gene SWISSPROT-<br>ID:Q99715 COLLAGEN ALPHA 1(XII)<br>CHAIN PRECURSOR - HOMO<br>SAPIENS (HUMAN), 3063<br>aa.   pds:SPTREMBL-ID:Q99715<br>COLLAGEN TYPE XII ALPHA-1<br>PRECURSOR - HOMO SAPIENS<br>(HUMAN), 3063 aa.                                       | 0.00E+00 | 6               |
| 11 | cg43933757 | 3195 | TCATCTCCCTGC<br>AACCTCCGCCT<br>CC[T]C]GGGTTT<br>AAGCGATTCTTG<br>TGCCTCA    | T | C   |  |  | SILENT-<br>NONCODING | complement       | Human Gene SWISSPROT-<br>ID:P10643 COMPLEMENT<br>COMPONENT C7 PRECURSOR -<br>HOMO SAPIENS (HUMAN), 843 aa.  | 0.00E+00 | 5 (5p13)        |
| 12 | cg43933757 | 3212 | CCGCCTCCTGG<br>GTTCAAGCGATT<br>CTT[T]C]GTGCCT<br>CAGCCTCCCAA<br>GCAGCTGG   | T | C   |  |  | SILENT-<br>NONCODING | complement       | Human Gene SWISSPROT-<br>ID:P10643 COMPLEMENT<br>COMPONENT C7 PRECURSOR -<br>HOMO SAPIENS (HUMAN), 843 aa.  | 0.00E+00 | 5 (5p13)        |

|    |            |      |   |   |     |  |  |                      |                |   |           |          |
|----|------------|------|---|---|-----|--|--|----------------------|----------------|---|-----------|----------|
| 13 | cg43933757 | 3346 | TCCAACCTCCTGA<br>CCTCAGGTAATC<br>C[G/A]CCTGCCT<br>TGGCCTCCCAA<br>AGTGCTG  | G | A   |  |  | SILENT-<br>NONCODING | complem<br>ent | Human Gene SWISSPROT-<br>ID:P10643 COMPLEMENT<br>COMPONENT C7 PRECURSOR -<br>HOMO SAPIENS (HUMAN), 843 aa.  | 0.00E+00  | 5 (5p13) |
| 14 | cg42185571 | 2224 | CTTAGCTCTACG<br>ATTAAATCCAT<br>G[T/gap]GTCCAA<br>GGGGGAAACA<br>TATTATAT   | T | gap |  |  | SILENT-<br>NONCODING | complem<br>ent | Human Gene SWISSPROT-<br>ID:P02748 COMPLEMENT<br>COMPONENT C9 PRECURSOR -<br>HOMO SAPIENS (HUMAN), 559 aa.  | 7.70E-308 | 5 (5p13) |
| 15 | cg42185571 | 2367 | TAATATAGATAG<br>TGTTCACTAGCA<br>G[A/gap]ATAGAA<br>TGAACATAAACT<br>ATTAGTT | A | gap |  |  | SILENT-<br>NONCODING | complem<br>ent | Human Gene SWISSPROT-<br>ID:P02748 COMPLEMENT<br>COMPONENT C9 PRECURSOR -<br>HOMO SAPIENS (HUMAN), 559 aa.  | 7.70E-308 | 5 (5p13) |
| 16 | cg43947909 | 265  | GAATTGTCCAGA<br>AGACTTGGCTC<br>AGC[T]TGGAGG<br>AGCTGATAGAC<br>ATGGCTGT    | C | T   |  |  | SILENT-<br>NONCODING | complem<br>ent | Human Gene Homologous to<br>SWISSPROT-ID:Q07021<br>COMPLEMENT COMPONENT 1, Q<br>SUBCOMPONENT BINDING<br>PROTEIN PRECURSOR<br>(GLYCOPROTEIN GC1QBP) (GC1Q-<br>R PROTEIN) (HYALURONAN-<br>BINDING PROTEIN 1) (PRE-MRNA<br>SPLICING FACTOR SF2, P32<br>SUBUNIT) - HOMO SAPIENS<br>(HUMAN), 282 aa. | 6.9E-129  | 17       |



|    |            |      |   |   |     |  |  |                      |            |  |          |               |
|----|------------|------|---|---|-----|--|--|----------------------|------------|--|----------|---------------|
| 17 | cg43143315 | 2860 | GTGTGTGTGTCT<br>GTGTGTGTGTG<br>TC[C/G]GTGTAT<br>GTGTGTGTGGG<br>TTCTAATG   | C | G   |  |  | SILENT-<br>NONCODING | cyto450    | Human Gene SWISSNEW-ID:Q07973<br>CYTOCHROME P450-CC24<br>MITOCHONDRIAL PRECURSOR (EC 1.14.-.) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa.lpcis:SWISSPROT-ID:Q07973<br>CYTOCHROME P450-CC24<br>MITOCHONDRIAL PRECURSOR (EC 1.14.-.) (P450- CC24) (VITAMIN D(3) 24-HYDROXYLASE) (1,25-DIHYDROXYVITAMIN D(3) 24-HYDROXYLASE) (24-OHASE) - HOMO SAPIENS (HUMAN), 513 aa. | 1.9E-279 | 20            |
| 18 | cg43327428 | 1746 | AGCAGGCTGGC<br>CTATGTGGTCTA<br>AG[A/G]TTCAGC<br>CTGAAACTCATA<br>GACACTG   | A | G   |  |  | SILENT-<br>NONCODING | cyto450    | Human Gene SWISSNEW-ID:P04798<br>CYTOCHROME P450 1A1 (EC 1.14.14.1) (CYP1A1) (P450-P1) (P450 FORM 6) (P450-C) - HOMO SAPIENS (HUMAN), 512 aa.lpcis:SWISSPROT-ID:P04798<br>CYTOCHROME P450 1A1 (EC 1.14.14.1) (P450-P1) (P450 FORM 6) (P450-C) (TCDD-INDUCIBLE) - HOMO SAPIENS (HUMAN).512 aa.  | 2.5E-279 | 15<br>(15q22) |
| 19 | cg32296860 | 376  | CAGCACTTTGG<br>GAGGCCGAGGC<br>GGG[T/C]GGATC<br>ACCCGAGGTCA<br>GGAGTTCCA   | T | C   |  |  | SILENT-<br>NONCODING | cytochrome | Human Gene Homologous to SPTREMBL-ID:Q27524<br>CYTOCHROME C OXIDASE<br>POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).   | 6.6E-124 |               |
| 20 | cg32296860 | 383  | TTGGGAGGCCG<br>AGCGGGGTGGA<br>TCA[C/gap]CCGA<br>GGTCAGGAGTT<br>CGAGACCAGC | C | gap |  |  | SILENT-<br>NONCODING | cytochrome | Human Gene Homologous to SPTREMBL-ID:Q27524<br>CYTOCHROME C OXIDASE<br>POLYPEPTIDE II (EC 1.9.3.1) - CAENORHABDITIS ELEGANS, 1647 aa (fragment).   | 6.6E-124 |               |



|    |            |     |   |   |   |  |  |  |                      |                   |   |                        |    |
|----|------------|-----|---|---|---|--|--|--|----------------------|-------------------|---|------------------------|----|
| 27 | cg43998926 | 560 | CTCAGGCTGAG<br>TTGCCTCCAATG<br>TTT/GJGGAATG<br>TCATCTTATACT<br>GGTACTG  | T | G |  |  |  | SILENT-<br>NONCODING | dehydrog<br>enase | Human Gene SWISSPROT-<br>ID:P50213 ISOCITRATE<br>DEHYDROGENASE (NAD),<br>MITOCHONDRIAL SUBUNIT ALPHA<br>PRECURSOR (EC 1.1.1.41)<br>(ISOCITRIC DEHYDROGENASE)<br>(NAD+-SPECIFIC ICDH) - HOMO<br>SAPIENS (HUMAN), 366 aa. | 1.30E-190              | 15 |
| 28 | cg43941594 | 499 | GGTTATAAAAT<br>AGATAACTCGCA<br>G/A/GJGTCATAA<br>ATATCTACAGTT<br>AGTAGA  | A | G |  |  |  | SILENT-<br>NONCODING | dehydrog<br>enase | Human Gene Homologous to<br>SWISSPROT-ID:P13707 GLYCEROL-<br>3-PHOSPHATE DEHYDROGENASE<br>(NAD+), CYTOPLASMIC (EC 1.1.1.8)<br>(GPD-C) (GPDH-C) - MUS<br>MUSCULUS (MOUSE), 348 aa.                                       | 1.90E-137              | 3  |
| 29 | cg43962927 | 462 | GCCACTCCCTG<br>CTCCCTGCCTG<br>AGC/G/AJCCATT<br>CGCAGTCTTGTT<br>TCCTGTTT | G | A |  |  |  | SILENT-<br>NONCODING | dna_rna<br>_bind  | Human Gene SWISSPROT-<br>ID:P38935 DNA-BINDING PROTEIN<br>SMUBP-2 (GLIAL FACTOR-1) (GF-1)<br>HOMO SAPIENS (HUMAN), 993 aa.  | 0.00E+00<br>(11q13.2 ) | 11 |
| 30 | cg43991661 | 671 | CTTGTTTATTAT<br>CTATCATAGACA<br>T/C/GJAAGATGA<br>TCATAGTTAATA<br>CCAATT | C | G |  |  |  | SILENT-<br>NONCODING | dna_rna<br>_bind  | Human Gene TREMBLNEW-<br>ID:G2058493 TELOMERIC REPEAT<br>DNA-BINDING PROTEIN - HOMO<br>SAPIENS (HUMAN), 419 aa.   | 5.10E-224              | 8  |
| 31 | cg43991661 | 737 | ACTGTTTATAGGC<br>CCAATATTGATA<br>T/A/GJTAAATGA<br>AGGTATCAGAG<br>AATCTT | A | G |  |  |  | SILENT-<br>NONCODING | dna_rna<br>_bind  | Human Gene TREMBLNEW-<br>ID:G2058493 TELOMERIC REPEAT<br>DNA-BINDING PROTEIN - HOMO<br>SAPIENS (HUMAN), 419 aa.   | 5.10E-224              | 8  |
| 32 | cg43310449 | 206 | CTAAAGATTTC<br>TGCTCTCAGTGG<br>A/A/GJCTGGCAT<br>ACTGTAATTGCT<br>ATGTGG  | A | G |  |  |  | SILENT-<br>NONCODING | dynein            | Human Gene SWISSPROT-<br>ID:Q63100 DYNEIN INTERMEDIATE<br>CHAIN 1, CYTOSOLIC (DH IC-1) -<br>RATTUS NORVEGICUS (RAT), 643<br>aa.   | 1.0e-312               |    |
| 33 | cg43310449 | 231 | ACTGGCATACT<br>GTAATTGCTATG<br>TG[G/A]AACTTAA<br>TATAACCTCAAC<br>AGCAGC | G | A |  |  |  | SILENT-<br>NONCODING | dynein            | Human Gene SWISSPROT-<br>ID:Q63100 DYNEIN INTERMEDIATE<br>CHAIN 1, CYTOSOLIC (DH IC-1) -<br>RATTUS NORVEGICUS (RAT), 643<br>aa.   | 1.0e-312               |    |



|    |            |      |  |   |     |  |  |  |                      |              |   |          |   |
|----|------------|------|--|---|-----|--|--|--|----------------------|--------------|---|----------|---|
| 41 | cg4398092  | 658  | TAGCGATACAAA<br>TATATATATAT<br>[A/gap]TTTATCC<br>AAAAATATGTTT<br>TATACA    | A | gap |  |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene SWISSPROT-<br>ID:Q01685 TRAM PROTEIN<br>(TRANSLOCATING CHAIN-<br>ASSOCIATING MEMBRANE<br>PROTEIN) - CANIS FAMILIARIS<br>(DOG), 373 aa. | 4E-192   | 8 |
| 42 | cg43953517 | 2457 | AAGTTCTTGTAG<br>TAGGTAGGGG<br>TA[C/T]TACTAGG<br>GATATCTGTGG<br>CATGATT     | C | T   |  |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene Homologous to<br>SWISSPROT-ID:P51674<br>MEMBRANE GLYCOPROTEIN M6-A -<br>HOMO SAPIENS (HUMAN), 278 aa.                                  | 2.9E-150 | 4 |
| 43 | cg43953517 | 2464 | TGTAGTAGGTA<br>GGGGGTACTAC<br>TAG[G/C]GATAT<br>CTGTGGCATGA<br>TTATGCAIT    | G | C   |  |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene Homologous to<br>SWISSPROT-ID:P51674<br>MEMBRANE GLYCOPROTEIN M6-A -<br>HOMO SAPIENS (HUMAN), 278 aa.                                  | 2.9E-150 | 4 |
| 44 | cg43953517 | 2491 | ATATCTGTGGCA<br>TGATTATGCATT<br>C[C/gap]GTAGTA<br>TTATTTAAATTAAT<br>TTGGGG | C | gap |  |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene Homologous to<br>SWISSPROT-ID:P51674<br>MEMBRANE GLYCOPROTEIN M6-A -<br>HOMO SAPIENS (HUMAN), 278 aa.                                  | 2.9E-150 | 4 |
| 45 | cg43953517 | 2517 | GTAGTATTATT<br>AATTAATTTGGG<br>G[T/G]TCATTTTG<br>CTTCCTTTTCTT<br>TATGC     | T | G   |  |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene Homologous to<br>SWISSPROT-ID:P51674<br>MEMBRANE GLYCOPROTEIN M6-A -<br>HOMO SAPIENS (HUMAN), 278 aa.                                  | 2.9E-150 | 4 |
| 46 | cg43953517 | 2529 | AATTAATTTGGG<br>GTTCAATTTTGCT<br>T[C/gap]CTTTTC<br>TTTATGCTTAGA<br>TTATCTT | C | gap |  |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene Homologous to<br>SWISSPROT-ID:P51674<br>MEMBRANE GLYCOPROTEIN M6-A -<br>HOMO SAPIENS (HUMAN), 278 aa.                                  | 2.9E-150 | 4 |
| 47 | cg43953517 | 2530 | ATTAATTTGGGG<br>TTCATTTTGCTT<br>C[C/gap]TTTTCT<br>TTATGCTTAGAT<br>TATCTTA  | C | gap |  |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene Homologous to<br>SWISSPROT-ID:P51674<br>MEMBRANE GLYCOPROTEIN M6-A -<br>HOMO SAPIENS (HUMAN), 278 aa.                                  | 2.9E-150 | 4 |

|    |            |      |  |   |     |  |  |                      |              |   |         |                 |
|----|------------|------|--|---|-----|--|--|----------------------|--------------|---|---------|-----------------|
| 48 | cg43290087 | 1150 | CCTAACCTCTTG<br>GTAACGGTAGT<br>CC[T/C]GAGAGT<br>TCGCAGTGTC A<br>GTGAAATC | T | C   |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene Similar to SWISSPROT-<br>ID:P52166 MEMBRANE PROTEIN<br>SEL-12 - CAENORHABDITIS<br>ELEGANS, 461 aa.   | 1.7E-97 | 14<br>(14q24.3) |
| 49 | cg43294632 | 913  | AGTAGAGAGTA<br>GGGGTAAAGC<br>TGG[A/G]CATTG<br>CAAAAGGATTG<br>GTTTAAGAA   | A | G   |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene Similar to SWISSNEW-<br>ID:Q13361 MICROFIBRIL-<br>ASSOCIATED GLYCOPROTEIN 2<br>PRECURSOR (MAGP-2) (MP25) -<br>HOMO SAPIENS (HUMAN), 173<br>aa.   pcis:SWISSPROT-ID:Q13361<br>MICROFIBRIL-ASSOCIATED<br>GLYCOPROTEIN 2 PRECURSOR<br>(MAGP-2) - HOMO SAPIENS<br>(HUMAN), 173 aa. | 4.3E-92 | 12              |
| 50 | cg43056971 | 884  | GTTATTTGAAAA<br>ATACCTATTTTT<br>T[T/gap]CCAAAG<br>TGTGTAAAGAT<br>TGTTTTG | T | gap |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene Similar to SPTREMBL-<br>ID:O04711 P-GLYCOPROTEIN-2 -<br>ARABIDOPSIS THALIANA (MOUSE-<br>EAR CRESS), 1233 aa.   | 2.2E-72 | 1               |
| 51 | cg43976227 | 212  | TTCATGTGCAAG<br>CTAAGTTATTCC<br>T[C/A]TGGTCAAT<br>CCTCTCCATCTT<br>CTGGT  | C | A   |  |  | SILENT-<br>NONCODING | glycoprotein | Human Gene Similar to SPTREMBL-<br>ID:Q14245 ERYTHROID<br>MEMBRANE PROTEIN 4.1 - HOMO<br>SAPIENS (HUMAN), 641 aa.   | 2.6E-60 | 18              |
| 52 | cg43994600 | 1782 | CCTTGTTCCAC<br>TCTCCTTCATAT<br>C[C/T]AAGTCAT<br>CAACATCTGAA<br>TGAGAG    | C | T   |  |  | SILENT-<br>NONCODING | helicase     | Human Gene Similar to SWISSNEW-<br>ID:O70133 ATP-DEPENDENT RNA<br>HELICASE A (NUCLEAR DNA<br>HELICASE II) (NDH II) (DEAD BOX<br>PROTEIN 9) (MHEL-5) - MUS<br>MUSCULUS (MOUSE), 1380<br>aa.   pcis:TREMBLNEW-ID:G2961456<br>RNA HELICASE A - MUS<br>MUSCULUS (MOUSE), 1380 aa.             | 8.7E-67 | 14              |

|    |            |      |   |   |   |  |  |                      |            |   |   |   |
|----|------------|------|---|---|---|--|--|----------------------|------------|---|---|---|
| 53 | cg43925670 | 2481 | ATGTTCTTGTAT<br>TTTTTCCCATC<br>TTTCTACAGACA<br>TAAGTGAGCCT<br>CACTGG  | T | C |  |  | SILENT-<br>NONCODING | interferon | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.lpcis:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0 | 1 |
| 54 | cg43925670 | 2488 | TGTATTTTTC<br>CCATCTTTACAG<br>AIC/TJATAAGTGA<br>GCCTCACTGGA<br>AATTTT | C | T |  |  | SILENT-<br>NONCODING | interferon | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.lpcis:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0 | 1 |
| 55 | cg43925670 | 2501 | CATCTTTACAGA<br>CATAAGTGAGC<br>CTCTJACTGGA<br>AATTTTTCAC<br>AGTAGTC   | C | T |  |  | SILENT-<br>NONCODING | interferon | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.lpcis:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0 | 1 |

|    |            |      |  |   |   |  |  |  |                      |                |   |   |   |
|----|------------|------|--|---|---|--|--|--|----------------------|----------------|---|---|---|
| 56 | cg43925670 | 2507 | TACAGACATAAG<br>TGAGCCTCACT<br>GG[AG]AATTTT<br>TCAACAGTAGTC<br>CAGATC  | A | G |  |  |  | SILENT-<br>NONCODING | interfero<br>n | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.jpcls:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0 | 1 |
| 57 | cg43925670 | 2513 | CATAAGTGAGC<br>CTCACTGGAAAT<br>TTT[C]TTCAACA<br>GTAGTCCAGAT<br>CTTGAGA | T | C |  |  |  | SILENT-<br>NONCODING | interfero<br>n | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.jpcls:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0 | 1 |
| 58 | cg43925670 | 2551 | CCAGATCTTGA<br>GATCTTCAGAAA<br>TG[C]TAGGAAT<br>CAATGCTTATTT<br>GTGTGAG | C | T |  |  |  | SILENT-<br>NONCODING | interfero<br>n | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.jpcls:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0 | 1 |



|    |            |      |  |   |     |  |  |                      |                      |   |          |                 |
|----|------------|------|--|---|-----|--|--|----------------------|----------------------|---|----------|-----------------|
| 59 | cg42489232 | 2434 | ATTTTGTAGTAGA<br>GACAAAGTTTGG<br>CCTTATGTTGG<br>CCAGGCTGGTC<br>TCGAACT   | C | T   |  |  | SILENT-<br>NONCODING | interferon           | Human Gene SWISSPROT-<br>ID:P48551 INTERFERON-<br>ALPHA/BETA RECEPTOR BETA<br>CHAIN PRECURSOR (IFN-ALPHA-<br>REC) (TYPE I INTERFERON<br>RECEPTOR) (IFN-R) (INTERFERON<br>ALPHA/BETA RECEPTOR- 2) -<br>HOMO SAPIENS (HUMAN), 515 aa. | 3.9E-281 | 21<br>(21q22.1) |
| 60 | cg42489232 | 2441 | GTAGAGACAAG<br>GTTTGGCCATGT<br>TG[G/C]CCAGGC<br>TGGTCTCGAACT<br>CCTGACC  | G | C   |  |  | SILENT-<br>NONCODING | interferon           | Human Gene SWISSPROT-<br>ID:P48551 INTERFERON-<br>ALPHA/BETA RECEPTOR BETA<br>CHAIN PRECURSOR (IFN-ALPHA-<br>REC) (TYPE I INTERFERON<br>RECEPTOR) (IFN-R) (INTERFERON<br>ALPHA/BETA RECEPTOR- 2) -<br>HOMO SAPIENS (HUMAN), 515 aa. | 3.9E-281 | 21<br>(21q22.1) |
| 61 | cg42489232 | 2454 | TTTGCCATGTTG<br>GCCAGGCTGGT<br>CTC[T/G]AACTC<br>CTGACCTCAAG<br>CGATCOGC  | C | T   |  |  | SILENT-<br>NONCODING | interferon           | Human Gene SWISSPROT-<br>ID:P48551 INTERFERON-<br>ALPHA/BETA RECEPTOR BETA<br>CHAIN PRECURSOR (IFN-ALPHA-<br>REC) (TYPE I INTERFERON<br>RECEPTOR) (IFN-R) (INTERFERON<br>ALPHA/BETA RECEPTOR- 2) -<br>HOMO SAPIENS (HUMAN), 515 aa. | 3.9E-281 | 21<br>(21q22.1) |
| 62 | cg43926168 | 694  | GAAGGGCTCTC<br>CTTCACGGGA<br>CTG[A/gap]AAAA<br>AAAAAATCATGA<br>AATCCTAAT | A | gap |  |  | SILENT-<br>NONCODING | interleukin receptor | Human Gene Similar to SWISSPROT-<br>ID:P18510 INTERLEUKIN-1<br>RECEPTOR ANTAGONIST PROTEIN<br>PRECURSOR (IL-1RA) (ICIL- 1RA)<br>(IRAP) - HOMO SAPIENS (HUMAN),<br>177 aa.   | 8.8E-94  | 2<br>(2q14.2)   |
| 63 | cg43926168 | 704  | CCTTCACGGGG<br>ACTGAAAAAAA<br>AA[A/gap]TCATG<br>AAATCCTAATTT<br>TCATTTTC | A | gap |  |  | SILENT-<br>NONCODING | interleukin receptor | Human Gene Similar to SWISSPROT-<br>ID:P18510 INTERLEUKIN-1<br>RECEPTOR ANTAGONIST PROTEIN<br>PRECURSOR (IL-1RA) (ICIL- 1RA)<br>(IRAP) - HOMO SAPIENS (HUMAN),<br>177 aa.   | 8.8E-94  | 2<br>(2q14.2)   |

|    |            |      |  |   |   |  |  |                      |        |  |           |    |
|----|------------|------|--|---|---|--|--|----------------------|--------|--|-----------|----|
| 64 | cg43336163 | 2889 | AGCCGGGAATG<br>CTGCTGCTGCT<br>GCT[G]A]CTGCT<br>GCTGCTGCTGC<br>TGGGGGGAT  | G | A |  |  | SILENT-<br>NONCODING | kinase | Human Gene TREMBLNEW-<br>ID:G300258 MYOTONIC<br>DYSTROPHY KINASE, DM-KINASE<br>{C-TERMINAL, ALTERNATIVELY<br>SPLICED, CLONE DELTA II} - HOMO<br>SAPIENS, 616 aa. | 0         | 19 |
| 65 | cg43987164 | 1043 | AGGCGAGCCCC<br>TCAGAAGCCTTC<br>CC[G]A]GCAGAT<br>CCGGGGACCCCC<br>GTTCTGGT | G | A |  |  | SILENT-<br>NONCODING | kinase | Human Gene TREMBLNEW-<br>ID:D1023392 INOSITOL 1,4,5-<br>TRISPHOSPHATE 3-KINASE<br>ISOENZYME (EC 2.7.1.127) - HOMO<br>SAPIENS (HUMAN), 604 aa<br>(fragment).      | 1.3E-307  |    |
| 66 | cg43119489 | 2227 | TTTTTCATCCTA<br>TCAATTGAATGT<br>G[G]C]CTTGAAA<br>AATCCAGCAAG<br>AGCGGGG  | G | C |  |  | SILENT-<br>NONCODING | kinase | Human Gene SWISSPROT-<br>ID:Q00537 SERINE/THREONINE-<br>PROTEIN KINASE PCTAIRE-2 (EC<br>2.7.1.-) - HOMO SAPIENS (HUMAN),<br>523 aa.                              | 2.7E-282  |    |
| 67 | cg43957170 | 2164 | CTACTAAAATA<br>CAAAAAATTAGC<br>C[G]A]GGCGTGG<br>TGGCGCATGCC<br>TGTAATC   | G | A |  |  | SILENT-<br>NONCODING | kinase | Human Gene SPTREMBL-ID:Q61399<br>CYCLIN-DEPENDENT PROTEIN<br>KINASE - MUS MUSCULUS<br>(MOUSE), 783 aa.   | 1.7E-234  |    |
| 68 | cg43957170 | 2175 | ACAAAAAATTAG<br>CCGGGCGTGGT<br>GG[C]T]GCATGC<br>CTGTAGTCCCA<br>GCTACTCG  | C | T |  |  | SILENT-<br>NONCODING | kinase | Human Gene SPTREMBL-ID:Q61399<br>CYCLIN-DEPENDENT PROTEIN<br>KINASE - MUS MUSCULUS<br>(MOUSE), 783 aa.   | 1.70E-234 |    |
| 69 | cg43957170 | 2179 | AAAATTAGCCG<br>GGCGTGGTGGC<br>GCA[T]C]GCCTG<br>TAGTCCCAGCTA<br>CTCGGGAG  | T | C |  |  | SILENT-<br>NONCODING | kinase | Human Gene SPTREMBL-ID:Q61399<br>CYCLIN-DEPENDENT PROTEIN<br>KINASE - MUS MUSCULUS<br>(MOUSE), 783 aa.   | 1.70E-234 |    |

|    |            |      |   |   |     |  |  |  |                      |        |   |           |    |
|----|------------|------|---|---|-----|--|--|--|----------------------|--------|---|-----------|----|
| 70 | cg38438124 | 1767 | ACTTTGTGTATA<br>TGTGTGTGTGT<br>GT[G/gap]TGTGT<br>GGGGGGGGTGA<br>GTGTGTGCG | G | gap |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SWISSNEW-ID:O70172<br>PHOSPHATIDYLINOSITOL-4-<br>PHOSPHATE 5-KINASE TYPE II<br>ALPHA (EC 2.7.1.68) (PIP5KII-<br>ALPHA) (1-<br>PHOSPHATIDYLINOSITOL-4-<br>PHOSPHATE KINASE) (PTDINS(4)P-<br>5-KINASE B ISOFORM)<br>(DIPHOSPHOINOSITIDE KINASE) -<br>MUS MUSCULUS (MOUSE), 405 aa. | 2.80E-216 | 10 |
| 71 | cg38438124 | 1769 | TTTGTGTATATG<br>TGTGTGTGTGT<br>GT[G/gap]TTGGG<br>GGGGGTGAGT<br>GTGTGCGCG  | G | gap |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SWISSNEW-ID:O70172<br>PHOSPHATIDYLINOSITOL-4-<br>PHOSPHATE 5-KINASE TYPE II<br>ALPHA (EC 2.7.1.68) (PIP5KII-<br>ALPHA) (1-<br>PHOSPHATIDYLINOSITOL-4-<br>PHOSPHATE KINASE) (PTDINS(4)P-<br>5-KINASE B ISOFORM)<br>(DIPHOSPHOINOSITIDE KINASE) -<br>MUS MUSCULUS (MOUSE), 405 aa. | 2.80E-216 | 10 |
| 72 | cg42923882 | 123  | AGTGGGCAGGG<br>ACCCTGGGAGC<br>CTC[C/A]ATTCTC<br>AATGCCCCACC<br>CTTTACCT   | C | A   |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SPTREMBL-ID:Q92961<br>MAP KINASE KINASE MEK5B -<br>HOMO SAPIENS (HUMAN), 448 aa.   | 1.80E-196 |    |
| 73 | cg43948037 | 1031 | AAAGTTCTCGAA<br>ATGCTTCATCCC<br>C[G/A]ACAAAGC<br>AAATTTTCATGTC<br>CGTCAG  | G | A   |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SWISSPROT-<br>ID:Q00532 SERINE/THREONINE-<br>PROTEIN KINASE KIALRE (EC<br>2.7.1.-) - HOMO SAPIENS (HUMAN),<br>358 aa.  | 6.10E-189 |    |
| 74 | cg43948037 | 1106 | CTGTTGCTTTCC<br>CTGGGGGTGTC<br>AG[G/A]CTCACC<br>AGGGGAGTCAG<br>AATCTTCT   | G | A   |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SWISSPROT-<br>ID:Q00532 SERINE/THREONINE-<br>PROTEIN KINASE KIALRE (EC<br>2.7.1.-) - HOMO SAPIENS (HUMAN),<br>358 aa.  | 6.10E-189 |    |

|    |            |      |   |   |     |  |  |  |                      |        |  |           |    |
|----|------------|------|---|---|-----|--|--|--|----------------------|--------|--|-----------|----|
| 75 | cg43948037 | 1115 | TCCCTGGGGTG<br>TCCAGGCTCAC<br>CAG[G]GGAGT<br>CAGAATCTTCTG<br>GTTCTCCC   | G | C   |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SWISSPROT-<br>ID:Q00532 SERINE/THREONINE-<br>PROTEIN KINASE KIALRE (EC<br>2.7.1.-) - HOMO SAPIENS (HUMAN),<br>358 aa.   | 6.10E-189 |    |
| 76 | cg43948037 | 1124 | TGTCCAGGCTC<br>ACCAGGGGAGT<br>CAG[A]GATCTT<br>CTGGTTCTCCCT<br>TTTCATCA  | A | G   |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SWISSPROT-<br>ID:Q00532 SERINE/THREONINE-<br>PROTEIN KINASE KIALRE (EC<br>2.7.1.-) - HOMO SAPIENS (HUMAN),<br>358 aa.   | 6.10E-189 |    |
| 77 | cg43948037 | 1134 | CACCAGGGGAG<br>TCAGAAATCTTCT<br>GG[T]CTCTCCC<br>TTTTCATCAAGT<br>CTTCTAA | T | C   |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SWISSPROT-<br>ID:Q00532 SERINE/THREONINE-<br>PROTEIN KINASE KIALRE (EC<br>2.7.1.-) - HOMO SAPIENS (HUMAN),<br>358 aa.   | 6.10E-189 |    |
| 78 | cg42703622 | 2409 | TGTGGGTTGAC<br>AGATTTTAAAA<br>TA[G/C]AATTTAG<br>AGTATTGGGGT<br>TTTGT    | G | C   |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SPTREMBL-ID:Q12792<br>PROTEIN TYROSINE KINASE -<br>HOMO SAPIENS (HUMAN), 350 aa.  | 3.00E-187 | 12 |
| 79 | cg43336176 | 5568 | TGCTGCTGCTG<br>CTGCTGCTGGG<br>GGG[G/gap]ATCA<br>CAGACCATTCT<br>TTCTTCGG | G | gap |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SPTREMBL-ID:Q16205<br>MYOTONIN PROTEIN KINASE -<br>HOMO SAPIENS (HUMAN), 625 aa.  | 1.10E-164 | 19 |
| 80 | cg43982923 | 610  | ACGCAGGGGTC<br>CCCGCGGCCGC<br>CGC[G/A]ATGCA<br>GAAATACGAGA<br>AACTGGA   | G | A   |  |  |  | SILENT-<br>NONCODING | kinase | Human Gene SWISSPROT-<br>ID:P49615 CELL DIVISION PROTEIN<br>KINASE 5 (EC 2.7.1.-) (TAU<br>PROTEIN KINASE II CATALYTIC<br>SUBUNIT) (TPKII CATALYTIC<br>SUBUNIT) (KINASE PSSALRE)<br>(CRK6) - MUS MUSCULUS<br>(MOUSE), 292 aa. | 3.60E-159 | 19 |

|    |            |      |  |   |   |  |  |  |                      |                    |   |           |    |
|----|------------|------|--|---|---|--|--|--|----------------------|--------------------|---|-----------|----|
| 81 | cg43265203 | 688  | ACATTCAAGCTC<br>GGTGTGTTTCA<br>C[A/C]CGCGTGC<br>GCCCGGCTGC<br>GGCGGTG    | A | C |  |  |  | SILENT-<br>NONCODING | kinase             | Human Gene Homologous to<br>SWISSNEW-ID:P54619 5'-AMP-<br>ACTIVATED PROTEIN KINASE,<br>GAMMA-1 SUBUNIT (AMPK GAMMA-<br>1 CHAIN) - HOMO SAPIENS<br>(HUMAN), 331 aa.pcls:SWISSPROT-<br>ID:P54619 5'-AMP-ACTIVATED<br>PROTEIN KINASE, GAMMA-1<br>SUBUNIT (AMPK GAMMA CHAIN) -<br>HOMO SAPIENS (HUMAN), 331 aa.                           | 5.50E-124 |    |
| 82 | cg43966625 | 77   | CGCTGCCCGCG<br>CGGGGACACACA<br>ACC[A/C]AAGTC<br>GCGGCGGCCGC<br>AGCCATGCG | A | C |  |  |  | SILENT-<br>NONCODING | kinase             | Human Gene Similar to SWISSPROT-<br>ID:Q15119 [PYRUVATE<br>DEHYDROGENASE(LIPOAMIDE)]<br>KINASE ISOZYME 2 PRECURSOR<br>(EC 2.7.1.99) (PYRUVATE<br>DEHYDROGENASE KINASE<br>ISOFORM 2) - HOMO SAPIENS<br>(HUMAN), 407 aa.pcls:SPTREMBL-<br>ID:Q15119 PYRUVATE<br>DEHYDROGENASE KINASE -<br>HOMO SAPIENS (HUMAN), 407 aa.                 | 3.20E-89  | 17 |
| 83 | cg44004317 | 4772 | CACCACGATGC<br>GGACCCCACTG<br>CCC[G/A]GCTCG<br>ACCTCCTCGGG<br>AGGGGGGCG  | G | A |  |  |  | SILENT-<br>NONCODING | kinasere<br>ceptor | Human Gene SWISSNEW-ID:P04626<br>ERBB-2 RECEPTOR PROTEIN-<br>TYROSINE KINASE PRECURSOR<br>(EC 2.7.1.112) (P185ERBB2) (NEU<br>PROTO-ONCOGENE) (C-ERBB-2) -<br>HOMO SAPIENS (HUMAN), 1255<br>aa.pcls:SWISSPROT-ID:P04626<br>ERBB-2 RECEPTOR PROTEIN-<br>TYROSINE KINASE PRECURSOR<br>(EC 2.7.1.112) - HOMO SAPIENS<br>(HUMAN), 1255 aa. | 0.00E+00  |    |
| 84 | cg43925424 | 300  | TCGGGCGACAG<br>TCGCTGCTCCG<br>CGC[G/T]CGCGC<br>CCGGCGGCGCT<br>CCAGGTGCT  | G | T |  |  |  | SILENT-<br>NONCODING | kinesin            | Human Gene SWISSPROT-<br>ID:Q07866 KINESIN LIGHT CHAIN<br>(KLC) - HOMO SAPIENS (HUMAN),<br>569 aa.  | 1.90E-304 | 14 |



|    |            |      |  |   |   |  |  |  |                      |                |   |                             |                      |
|----|------------|------|--|---|---|--|--|--|----------------------|----------------|---|-----------------------------|----------------------|
| 89 | cg43263644 | 143  | GCCGGGACAGT<br>GTTGTACAGTGT<br>TTT[C]GGGCAT<br>GCACGTGATAC<br>TCACACAG       | T | C |  |  |  | SILENT-<br>NONCODING | nucl_rec<br>pt | Human Gene SWISSPROT-<br>ID:Q03181 PEROXISOME<br>PROLIFERATOR ACTIVATED<br>RECEPTOR BETA (PPAR-BETA)<br>(PPAR-DELTA) (NUCLEAR<br>HORMONE RECEPTOR 1) (NUC1)<br>(NUC1) - HOMO SAPIENS (HUMAN),<br>441 aa.  | 4.70E-237                   | 6                    |
| 90 | cg44131079 | 3497 | CGGTGATATTAC<br>AAAACAATGAAT<br>TTC[T]GGAACTAT<br>TATAGATTGGGC<br>ACCTC      | C | T |  |  |  | SILENT-<br>NONCODING | nuclease       | Human Gene SWISSNEW-ID:P10266<br>RETROVIRUS-RELATED POL<br>POLYPROTEIN [CONTAINS:<br>REVERSE TRANSCRIPTASE (EC<br>2.7.7.49); ENDONUCLEASE] -<br>HOMO SAPIENS (HUMAN), 874<br>aa.lpcds:SWISSPROT-ID:P10266<br>RETROVIRUS-RELATED POL<br>POLYPROTEIN (REVERSE<br>TRANSCRIPTASE (EC 2.7.7.49);<br>ENDONUCLEASE) - HOMO<br>SAPIENS (HUMAN), 874 aa. | 0.00E+00                    |                      |
| 91 | cg44031914 | 153  | GCACAGGGGAG<br>TGAGGGCAGGG<br>CGC[T/C]CGCAG<br>GGGGCACGCAG<br>GGAGGGCCC      | T | C |  |  |  | SILENT-<br>NONCODING | oncogene       | Human Gene SWISSPROT-<br>ID:Q01543 FLI-1 ONCOGENE (ERGB<br>TRANSCRIPTION FACTOR) - HOMO<br>SAPIENS (HUMAN), 452 aa.   | 4.70E-253                   | 11<br>(11q24)        |
| 92 | cg43932550 | 3136 | CATCATAGAACT<br>CCTTGTGGATCT<br>CIG[A/T]AGAGCT<br>CAGGCACTTTG<br>AAGAAGA     | G | A |  |  |  | SILENT-<br>NONCODING | oncogene       | Human Gene SPTREMBL-ID:Q13746<br>BCR-ABL MRNA OF ACUTE<br>LYMPHOCTIC LEUKAEMIA (ALL)<br>PATIENTS - HOMO SAPIENS<br>(HUMAN), 386 aa.   | 2.30E-205<br>(22q11.2<br>1) | 22<br>(22q11.2<br>1) |
| 93 | cg43932550 | 3312 | GACAGGACCCA<br>A<br>TTTTCTCATCTC<br>CA[A/G]GCCCTT<br>TTCCAAGTCCAG<br>CTCACTC | A | G |  |  |  | SILENT-<br>NONCODING | oncogene       | Human Gene SPTREMBL-ID:Q13746<br>BCR-ABL MRNA OF ACUTE<br>LYMPHOCTIC LEUKAEMIA (ALL)<br>PATIENTS - HOMO SAPIENS<br>(HUMAN), 386 aa.   | 2.30E-205<br>(22q11.2<br>1) | 22<br>(22q11.2<br>1) |

|    |            |      |  |   |     |  |  |                      |             |  |           |          |
|----|------------|------|--|---|-----|--|--|----------------------|-------------|--|-----------|----------|
| 94 | cg43967268 | 598  | ACGAGAAAGG<br>AGCAGCTGAA<br>GTG[G]CCTGG<br>ACTCCAGCCCT<br>GGCTGTTGT              | G | A   |  |  | SILENT-<br>NONCODING | oncogene    | Human Gene Similar to SWISSPROT-<br>ID:P24407 RAS-RELATED PROTEIN<br>RAB-8 (ONCOGENE C-MEL) -<br>HOMO SAPIENS (HUMAN), AND<br>CANIS FAMILIARIS (DOG), 207 aa.  | 1.90E-52  |          |
| 95 | cg43920534 | 1076 | CGTCACTATGTA<br>CTTGGTTTTGCG<br>CT[ <i>gap</i> ]TTTTTTT<br>CCTTAAAAAAA<br>AAGGCC | T | gap |  |  | SILENT-<br>NONCODING | phosphatase | Human Gene SPTREMBL-ID:Q10728<br>SERINE/THREONINE PROTEIN<br>PHOSPHATASE PP1 SMOOTH<br>MUSCLE REGULATORY M110<br>SUBUNIT (110 KDA SUBUNIT) -<br>RATTUS NORVEGICUS (RAT), 976<br>aa.  | 0.00E+00  | 12       |
| 96 | cg43920534 | 763  | CTTCATAAAACC<br>AATCGAGAGAG<br>AG[A] <i>gap</i> GGACT<br>TAAATCCTGCT<br>TACCAAAA | A | gap |  |  | SILENT-<br>NONCODING | phosphatase | Human Gene SPTREMBL-ID:Q10728<br>SERINE/THREONINE PROTEIN<br>PHOSPHATASE PP1 SMOOTH<br>MUSCLE REGULATORY M110<br>SUBUNIT (110 KDA SUBUNIT) -<br>RATTUS NORVEGICUS (RAT), 976<br>aa.  | 0.00E+00  | 12       |
| 97 | cg43926887 | 1786 | ATTGTTTTCAAC<br>ATGAAGTAAAGA<br>A[T]A[A]ACGTTGA<br>GGCCTTTACTAT<br>TAGCT         | T | A   |  |  | SILENT-<br>NONCODING | phosphatase | Human Gene SWISSPROT-<br>ID:Q06190 PROTEIN<br>PHOSPHATASE PP2A, 130 KD<br>REGULATORY SUBUNIT (PR130) -<br>HOMO SAPIENS (HUMAN), 1150 aa.   | 0.00E+00  | 3        |
| 98 | cg43926887 | 1838 | GTCTAATACTCC<br>TGGGAGGAAGG<br>AA[T]A]ATATCTA<br>TCTAGTAAGAAT<br>TTTAAT          | T | A   |  |  | SILENT-<br>NONCODING | phosphatase | Human Gene SWISSPROT-<br>ID:Q06190 PROTEIN<br>PHOSPHATASE PP2A, 130 KD<br>REGULATORY SUBUNIT (PR130) -<br>HOMO SAPIENS (HUMAN), 1150 aa.   | 0.00E+00  | 3        |
| 99 | cg43088901 | 2303 | GAGCACCGTGT<br>CAAGCTGCTCT<br>GAG[C/T]CACAG<br>TGGGATGAACC<br>AGCCGGGGC          | C | T   |  |  | SILENT-<br>NONCODING | phosphatase | Human Gene SWISSNEW-ID:P30304<br>M-PHASE INDUCER<br>PHOSPHATASE 1 (EC 3.1.3.48) -<br>HOMO SAPIENS (HUMAN), 523<br>aa.<br>ipdls:SWISSPROT-ID:P30304 M-<br>PHASE INDUCER PHOSPHATASE 1<br>(EC 3.1.3.48) - HOMO SAPIENS<br>(HUMAN), 523 aa. | 4.00E-288 | 3 (3p21) |



|     |            |      |  |   |     |  |  |                      |                   |   |           |    |
|-----|------------|------|--|---|-----|--|--|----------------------|-------------------|---|-----------|----|
| 100 | cg43920213 | 3664 | GTGAGCCATAAT<br>ATGATGGCCAG<br>CA[G/gap]GTGG<br>CGCTGCCCTTCC<br>ACCCATGGTG | G | gap |  |  | SILENT-<br>NONCODING | phosphatase       | Human Gene Similar to SWISSPROT-<br>ID:P51452 DUAL SPECIFICITY<br>PROTEIN PHOSPHATASE 3 (EC<br>3.1.3.48) (EC 3.1.3.16) (DUAL<br>SPECIFICITY PROTEIN<br>PHOSPHATASE VHR) - HOMO<br>SAPIENS (HUMAN), 185 aa.  | 6.00E-81  | 17 |
| 101 | cg43969348 | 648  | TGGGGGAAATG<br>GGCCTCTTGGG<br>GGT[C/gap]TCAC<br>TGCACGGCTTG<br>TTCATTGGCA  | C | gap |  |  | SILENT-<br>NONCODING | polymrase         | Human Gene Similar to SPTREMBL-<br>ID:Q15370 RNA POLYMERASE II<br>TRANSCRIPTION FACTOR SIII P18<br>SUBUNIT - HOMO SAPIENS<br>(HUMAN), 118 aa.   | 3.90E-59  | 16 |
| 102 | cg43966692 | 331  | TACGAATTGGCA<br>TATTTGTTTATTT<br>[C/gap]TCAGTTT<br>GTGAAAATGTCC<br>TTAATT  | C | gap |  |  | SILENT-<br>NONCODING | polymrase         | Human Gene Similar to SPTREMBL-<br>ID:Q15369 RNA POLYMERASE II<br>ELONGATION FACTOR SIII, P15<br>SUBUNIT - HOMO SAPIENS<br>(HUMAN), 112 aa.   | 4.00E-57  | 8  |
| 103 | cg43265754 | 4375 | CGAGACCAGCC<br>TGGCCAACATG<br>GTG[A/C]AACCC<br>CATCTCTACTAA<br>AAATACAA    | A | C   |  |  | SILENT-<br>NONCODING | potassium_channel | Human Gene SWISSPROT-<br>ID:P48544 G PROTEIN-ACTIVATED<br>INWARD RECTIFIER POTASSIUM<br>CHANNEL 4 (GIRK4) (POTASSIUM<br>CHANNEL, INWARDLY<br>RECTIFYING, SUBFAMILY J,<br>MEMBER 5) (HEART KATP<br>CHANNEL) (KATP-1) (CARDIAC<br>INWARD RECTIFIER) (CIR) (KIR3.4) -<br>HOMO SAPIENS (HUMAN), 419 aa. | 6.70E-185 |    |
| 104 | cg43265754 | 4389 | CCAACATGGTG<br>AAACCCCATCTC<br>TA[C/T]TAAAAAT<br>ACAAAAATTAGC<br>CGGGCG    | C | T   |  |  | SILENT-<br>NONCODING | potassium_channel | Human Gene SWISSPROT-<br>ID:P48544 G PROTEIN-ACTIVATED<br>INWARD RECTIFIER POTASSIUM<br>CHANNEL 4 (GIRK4) (POTASSIUM<br>CHANNEL, INWARDLY<br>RECTIFYING, SUBFAMILY J,<br>MEMBER 5) (HEART KATP<br>CHANNEL) (KATP-1) (CARDIAC<br>INWARD RECTIFIER) (CIR) (KIR3.4) -<br>HOMO SAPIENS (HUMAN), 419 aa. | 6.70E-185 |    |

|     |            |      |   |   |     |  |  |  |                      |               |   |           |                 |
|-----|------------|------|---|---|-----|--|--|--|----------------------|---------------|---|-----------|-----------------|
| 105 | cg43922227 | 538  | ATGTTGTGTTGG<br>GTCCCCAGATT<br>CC[C/T]ATTGAT<br>TTTCTTGCATCA<br>TTTTCT    | C |     |  |  |  | SILENT-<br>NONCODING | reductas<br>e | Human Gene Homologous to<br>SWISSPROT-ID:P36959 GMP<br>REDUCTASE (EC 1.6.6.8)<br>(GUANOSINE 5'-MONOPHOSPHATE<br>OXIDOREDUCTASE) - HOMO<br>SAPIENS (HUMAN), 345 aa.  | 7.70E-150 | 14              |
| 106 | cg43927549 | 1020 | GTAAGCAGCAC<br>ACTAGGAGGCC<br>CAG[G/gap]CGC<br>AGGCAAAGAGA<br>AGATGGTGCTG | G | gap |  |  |  | SILENT-<br>NONCODING | reductas<br>e | Human Gene Homologous to<br>SWISSPROT-ID:P16083 NAD(P)H<br>DEHYDROGENASE (QUINONE) 2<br>(EC 1.6.99.2) (QUINONE<br>REDUCTASE) (DT-DIAPHORASE)<br>(AZOREDUCTASE)<br>(PHYLLOQUINONE REDUCTASE)<br>(MENADIONE REDUCTASE) -<br>HOMO SAPIENS (HUMAN), 231 aa. | 1.60E-124 | 6 (6pter)       |
| 107 | cg43957486 | 4041 | TGTATCATAGAA<br>ATGTAACITTTTG<br>T[A/G]AGACAAA<br>GGTTTTCCTCTT<br>CTATTT  | A | G   |  |  |  | SILENT-<br>NONCODING | struct        | Human Gene SWISSPROT-<br>ID:P07204 THROMBOMODULIN<br>PRECURSOR (FETOMODULIN) (TM)<br>(CD141 ANTIGEN) - HOMO<br>SAPIENS (HUMAN), 575 aa.   | 0.00E+00  | 20<br>(20p11.2) |
| 108 | cg43973080 | 779  | GACACTAGGAA<br>TTTCTTAAAAAG<br>AA[A/gap]GATGT<br>TGGAAGCAGAA<br>CACTTACTA | A | gap |  |  |  | SILENT-<br>NONCODING | struct        | Human Gene TREMBLNEW-<br>ID:G2304981 MYOSIN VI - HOMO<br>SAPIENS (HUMAN), 1262 aa.  | 0.00E+00  | 6               |
| 109 | cg42914441 | 2306 | CTCTGACCTGA<br>GTCITTTGTTTAA<br>AG[A/G]AGTATTT<br>GTCITTCCTTTGT<br>CTAATG | A | G   |  |  |  | SILENT-<br>NONCODING | struct        | Human Gene Homologous to<br>SWISSPROT-ID:P26044 RADIXIN<br>(MOESIN B) - SUS SCROFA (PIG),<br>583 aa.  | 5.40E-133 | 22<br>(22q12.2) |
| 110 | cg43942318 | 1006 | GGACACCCCTCG<br>GACCCTCGAAA<br>ACG[C/T]CTCAG<br>GAGCTATGAAG<br>ACATGATTG  | C | T   |  |  |  | SILENT-<br>NONCODING | struct        | Human Gene Homologous to<br>SPTREMBL-ID:O00379 DELTA-<br>CATENIN - HOMO SAPIENS<br>(HUMAN), 792 aa.   | 4.80E-123 | 11              |

|     |            |      |   |   |     |  |  |                      |          |  |           |    |
|-----|------------|------|---|---|-----|--|--|----------------------|----------|--|-----------|----|
| 111 | cg43929933 | 431  | CAGGCCAGGCC<br>TGTTGTCTCCAC<br>CTG[C/G]ACAGG<br>CATTCTCCTTGT<br>TCCAGAAA  | C | G   |  |  | SILENT-<br>NONCODING | struct   | Human Gene Homologous to<br>SPTREMBL-ID:P97756<br>CA2+/CALMODULIN-DEPENDENT<br>PROTEIN KINASE IV KINASE<br>ISOFORM - RATTUS NORVEGICUS<br>(RAT), 505 aa.   | 1.80E-117 | 12 |
| 112 | cg43929933 | 541  | CGCAGCCCCAA<br>GTGTCAACAAG<br>GGG[C/T]TCAAT<br>AAGGCTTTCTG<br>GGAGCCACT   | C | T   |  |  | SILENT-<br>NONCODING | struct   | Human Gene Homologous to<br>SPTREMBL-ID:P97756<br>CA2+/CALMODULIN-DEPENDENT<br>PROTEIN KINASE IV KINASE<br>ISOFORM - RATTUS NORVEGICUS<br>(RAT), 505 aa.   | 1.80E-117 | 12 |
| 113 | cg43929933 | 590  | CTGGCAGCTGG<br>TGGGATGGAAG<br>GGG[G/gap]AGG<br>TGGAAAAGGGC<br>AGAGGAAATGG | G | gap |  |  | SILENT-<br>NONCODING | struct   | Human Gene Homologous to<br>SPTREMBL-ID:P97756<br>CA2+/CALMODULIN-DEPENDENT<br>PROTEIN KINASE IV KINASE<br>ISOFORM - RATTUS NORVEGICUS<br>(RAT), 505 aa.   | 1.80E-117 | 12 |
| 114 | cg43070037 | 7268 | AGGTCAGGAGT<br>TTGAGACCAGC<br>CTA[G/A]CCAAC<br>ATGGTGAAACC<br>CCATCTCTA   | G | A   |  |  | SILENT-<br>NONCODING | synthase | Human Gene SWISSPROT-<br>ID:P35421<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE (EC 6.3.5.3)<br>(FGAM SYNTHASE)<br>(FORMYLGLYCINAMIDE RIBOTIDE<br>AMIDOTRANSFERASE) (FGARAT)<br>(ADENOSINE-2) (FGAMS)<br>(FORMYLGLYCINAMIDE RIBOTIDE<br>SYNTHETASE) - DROSOPHILA<br>MELANOGASTER (FRUIT FLY),<br>1354 aa. | 0.00E+00  |    |

|     |            |      |   |   |   |  |  |  |                      |          |  |          |  |
|-----|------------|------|---|---|---|--|--|--|----------------------|----------|--|----------|--|
| 115 | cg43070037 | 7269 | GGTCAGGAGTT<br>TGAGACCAGCC<br>TAGC/GJCAACA<br>TGGTGAAACCC<br>CATCTCTAC  | C | G |  |  |  | SILENT-<br>NONCODING | synthase | Human Gene SWISSPROT-<br>ID:P35421<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE (EC 6.3.5.3)<br>(FGAM SYNTHASE)<br>(FORMYLGLYCINAMIDE RIBOTIDE<br>AMIDOTRANSFERASE) (FGARAT)<br>(ADENOSINE-2) (FGAMS)<br>(FORMYLGLYCINAMIDE RIBOTIDE<br>SYNTHETASE) - DROSOPHILA<br>MELANOGASTER (FRUIT FLY),<br>1354 aa. | 0.00E+00 |  |
| 116 | cg43070037 | 7352 | GIGGGTGCCTG<br>TAATCCCAGCTA<br>CT[C/T]GGGAGG<br>CTGAGGCAGGA<br>GAATCACC | C | T |  |  |  | SILENT-<br>NONCODING | synthase | Human Gene SWISSPROT-<br>ID:P35421<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE (EC 6.3.5.3)<br>(FGAM SYNTHASE)<br>(FORMYLGLYCINAMIDE RIBOTIDE<br>AMIDOTRANSFERASE) (FGARAT)<br>(ADENOSINE-2) (FGAMS)<br>(FORMYLGLYCINAMIDE RIBOTIDE<br>SYNTHETASE) - DROSOPHILA<br>MELANOGASTER (FRUIT FLY),<br>1354 aa. | 0.00E+00 |  |
| 117 | cg43070037 | 7365 | ATCCCAGCTACT<br>CGGGAGGCTGA<br>GG[C/T]AGGAGA<br>ATCACCTGAACC<br>TAGGAGG | C | T |  |  |  | SILENT-<br>NONCODING | synthase | Human Gene SWISSPROT-<br>ID:P35421<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE (EC 6.3.5.3)<br>(FGAM SYNTHASE)<br>(FORMYLGLYCINAMIDE RIBOTIDE<br>AMIDOTRANSFERASE) (FGARAT)<br>(ADENOSINE-2) (FGAMS)<br>(FORMYLGLYCINAMIDE RIBOTIDE<br>SYNTHETASE) - DROSOPHILA<br>MELANOGASTER (FRUIT FLY),<br>1354 aa. | 0.00E+00 |  |

|     |            |      |  |   |     |  |  |  |                      |                  |  |           |    |
|-----|------------|------|--|---|-----|--|--|--|----------------------|------------------|--|-----------|----|
| 118 | cg43070037 | 7366 | TCCAGCTACTCA<br>GGGAGGCTGAG<br>GC[A/G]GGAGAA<br>TCACCTGAACCT<br>AGGAGGC  | A | G   |  |  |  | SILENT-<br>NONCODING | synthase         | Human Gene SWISSPROT-<br>ID:P35421<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE (EC 6.3.5.3)<br>(FGAM SYNTHASE)<br>(FORMYLGLYCINAMIDE RIBOTIDE<br>AMIDOTRANSFERASE) (FGARAT)<br>(ADENOSINE-2) (FGAMS)<br>(FORMYLGLYCINAMIDE RIBOTIDE<br>SYNTHETASE) - DROSOPHILA<br>MELANOGASTER (FRUIT FLY),<br>1354 aa. | 0.00E+00  |    |
| 119 | cg43123664 | 240  | AGTACGCCAGC<br>CCGGGGCGGCC<br>CCG[A/C]ATGTA<br>CATGTTCCACG<br>CGGGATTCC  | A | C   |  |  |  | SILENT-<br>NONCODING | synthase         | Human Gene Similar to SWISSPROT-<br>ID:O35696 ALPHA-2,8-<br>SIALYLTRANSFERASE (EC 2.4.99.-)<br>(ST8SIAII) (SIALYLTRANSFERASE<br>X) (STX) (POLYSIALIC ACID<br>SYNTHASE) - MUS MUSCULUS<br>(MOUSE), 375 aa.  | 3.10E-59  | 18 |
| 120 | cg21428405 | 17   | NACGCGTTGGC<br>GTCGTT/CJCTC<br>GTTGAGCTCATC<br>AATCCACCAC                | T | C   |  |  |  | SILENT-<br>NONCODING | synthase         | Human Gene Similar to SWISSNEW-<br>ID:P54876<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE II (EC<br>6.3.5.3) (FGAM SYNTHASE II) -<br>MYCOBACTERIUM<br>TUBERCULOSIS, 754 aa.   | 2.20E-56  |    |
| 121 | cg43982633 | 811  | ACACAGCCCCA<br>GTTTGCTTTACA<br>GC[C/G]CAAGTT<br>ACAAACTGTCCC<br>TTTTAAA  | C | G   |  |  |  | SILENT-<br>NONCODING | tgfrecept<br>or  | Human Gene SWISSPROT-<br>ID:P56159 GDNF RECEPTOR<br>ALPHA PRECURSOR (GDNFR-<br>ALPHA) (TGF-BETA RELATED<br>NEUROTROPHIC FACTOR<br>RECEPTOR 1) - HOMO SAPIENS<br>(HUMAN), 464 aa.   | 1.50E-254 |    |
| 122 | cg43054268 | 312  | TCTAGATATTTA<br>ACTGACCCACTA<br>T[A/gap]TTCCTC<br>AAGGATACTGC<br>ATTGGAC | A | gap |  |  |  | SILENT-<br>NONCODING | thioester<br>ase | Human Gene Similar to<br>TREMBLNEW-ID:E307161<br>MITOCHONDRIAL VERY-LONG-<br>CHAIN ACYL-COA THIOESTERASE -<br>RATTUS NORVEGICUS (RAT), 453<br>aa.  | 3.50E-83  | 9  |

|     |            |      |  |   |     |  |  |                      |                  |   |           |          |
|-----|------------|------|--|---|-----|--|--|----------------------|------------------|---|-----------|----------|
| 123 | cg43054268 | 448  | GACTATATGATC<br>AAAGCCCTTAG<br>C[A]gapJAAAAA<br>ATTTTAAATATT<br>TGCAAA   | A | gap |  |  | SILENT-<br>NONCODING | thioester<br>ase | Human Gene Similar to<br>TREMBLNEW-ID:E307161<br>MITOCHONDRIAL VERY-LONG-<br>CHAIN ACYL-COA THIOESTERASE -<br>RATTUS NORVEGICUS (RAT), 453<br>aa.                   | 3.50E-83  | 9        |
| 124 | cg43943775 | 259  | TGAAGATTACCC<br>CCACACCTGTG<br>TG[A]GJCAAGTG<br>ATCAAAAAGGAA<br>CAGGACC  | A | G   |  |  | SILENT-<br>NONCODING | tm7              | Human Gene SWISSPROT-<br>ID:P21554 CANNABINOID<br>RECEPTOR 1 (CB1) (CB-R) (CANN6)<br>- HOMO SAPIENS (HUMAN), 472 aa.  | 5.40E-252 | 6 (6q14) |
| 125 | cg42886565 | 3473 | GGCAACAAAAG<br>CGAAACTCCATC<br>TC[A]gapJAAAA<br>AAAGAGCTATAG<br>GATCTTTA | A | gap |  |  | SILENT-<br>NONCODING | tm7              | Human Gene SWISSPROT-<br>ID:P25116 THROMBIN RECEPTOR<br>PRECURSOR - HOMO SAPIENS<br>(HUMAN), 425 aa.  | 4.40E-225 | 5 (5q13) |
| 126 | cg42886565 | 3481 | AAGCGAAACTC<br>CATCTCAAAAA<br>AA[A]gapJGAGCT<br>ATAGGATCTTTA<br>CAATATAI | A | gap |  |  | SILENT-<br>NONCODING | tm7              | Human Gene SWISSPROT-<br>ID:P25116 THROMBIN RECEPTOR<br>PRECURSOR - HOMO SAPIENS<br>(HUMAN), 425 aa.  | 4.40E-225 | 5 (5q13) |
| 127 | cg42886565 | 4462 | TCCTCTGTCTGC<br>TGGCTGGCCGC<br>GT[G]AJTAGAA<br>GAAGACTAATTG<br>GACACAG   | G | A   |  |  | SILENT-<br>NONCODING | tm7              | Human Gene SWISSPROT-<br>ID:P25116 THROMBIN RECEPTOR<br>PRECURSOR - HOMO SAPIENS<br>(HUMAN), 425 aa.  | 4.40E-225 | 5 (5q13) |
| 128 | cg42886565 | 4483 | GCGTGTATGAA<br>GAAGACTAATTG<br>GA[C]TJACAGAG<br>CCGTGATGAATT<br>AAAGTCT  | C | T   |  |  | SILENT-<br>NONCODING | tm7              | Human Gene SWISSPROT-<br>ID:P25116 THROMBIN RECEPTOR<br>PRECURSOR - HOMO SAPIENS<br>(HUMAN), 425 aa.  | 4.40E-225 | 5 (5q13) |
| 129 | cg43307001 | 1796 | GCCTCCCGGGT<br>TCAAGTGATTCT<br>CC[T]CJGCCTCA<br>GCCTCCCAGTA<br>GCTGGGAT  | T | C   |  |  | SILENT-<br>NONCODING | tm7              | Human Gene SWISSPROT-<br>ID:P35348 ALPHA-1A ADRENERGIC<br>RECEPTOR (ALPHA 1A-<br>ADRENOCEPTOR) (ALPHA-1C<br>ADRENERGIC RECEPTOR) - HOMO<br>SAPIENS (HUMAN), 466 aa. | 2.50E-199 |          |

|     |            |      |  |   |     |  |  |                      |     |   |           |    |
|-----|------------|------|--|---|-----|--|--|----------------------|-----|---|-----------|----|
| 130 | cg43307001 | 1898 | GGGGTTTCACC<br>ATGTTGGCCAG<br>GCT[G/A]GTCTC<br>GAACTCCTGAC<br>CTCAAGTGA  | G | A   |  |  | SILENT-<br>NONCODING | tm7 | Human Gene SWISSPROT-<br>ID:P35348 ALPHA-1A ADRENERGIC<br>RECEPTOR (ALPHA 1A-<br>ADRENOCEPTOR) (ALPHA-1C<br>ADRENERGIC RECEPTOR) - HOMO<br>SAPIENS (HUMAN), 466 aa. | 2.50E-199 |    |
| 131 | cg43307001 | 1909 | ATGTTGGCCAG<br>GCTGGTCTCGA<br>ACT[C/T]CTGAC<br>CTCAAGTGATCC<br>GCCACCT   | C | T   |  |  | SILENT-<br>NONCODING | tm7 | Human Gene SWISSPROT-<br>ID:P35348 ALPHA-1A ADRENERGIC<br>RECEPTOR (ALPHA 1A-<br>ADRENOCEPTOR) (ALPHA-1C<br>ADRENERGIC RECEPTOR) - HOMO<br>SAPIENS (HUMAN), 466 aa. | 2.50E-199 |    |
| 132 | cg43047341 | 2113 | GGTGGATCACC<br>TGAGGTCACGA<br>GTT[C/T]GAGAC<br>CAGCCTGACCA<br>ACATGGAGA  | C | T   |  |  | SILENT-<br>NONCODING | tm7 | Human Gene SWISSPROT-<br>ID:P21731 THROMBOXANE A2<br>RECEPTOR (TXA2-R)<br>(PROSTANOID TP RECEPTOR) -<br>HOMO SAPIENS (HUMAN), 369 aa.                               | 2.80E-190 |    |
| 133 | cg43965652 | 891  | TCCATTCTTTT<br>TCTTTTTTTTTT<br>[T/gap]TAAGTGA<br>GACTACATTGG<br>CAAATGG  | T | gap |  |  | SILENT-<br>NONCODING | tnf | Human Gene Homologous to<br>SPTREMBL-ID:Q99732 TNF-ALPHA<br>INDUCIBLE RESPONSIVE<br>ELEMENT - HOMO SAPIENS<br>(HUMAN), 228 aa.                                      | 4.50E-121 | 16 |
| 134 | cg43965652 | 892  | CCATTCTTTT<br>CTTTTTTTTTTT<br>[T/gap]AAGTGAG<br>ACTACATTGGCA<br>AATGGG   | T | gap |  |  | SILENT-<br>NONCODING | tnf | Human Gene Homologous to<br>SPTREMBL-ID:Q99732 TNF-ALPHA<br>INDUCIBLE RESPONSIVE<br>ELEMENT - HOMO SAPIENS<br>(HUMAN), 228 aa.                                      | 4.50E-121 | 16 |
| 135 | cg43965652 | 412  | TTCCAAACATCA<br>AATGAAGGGG<br>AT[C/gap]AATGG<br>TTACCACTATCG<br>TTTTCAAC | C | gap |  |  | SILENT-<br>NONCODING | tnf | Human Gene Homologous to<br>SPTREMBL-ID:Q99732 TNF-ALPHA<br>INDUCIBLE RESPONSIVE<br>ELEMENT - HOMO SAPIENS<br>(HUMAN), 228 aa.                                      | 4.50E-121 | 16 |
| 136 | cg43985709 | 933  | AGCTCACTTTGG<br>CCCTTCTCCACC<br>C[A/G]TCCCAAC<br>CCCAATTGCTAAC<br>AACATG | A | G   |  |  | SILENT-<br>NONCODING | tnf | Human Gene Similar to SWISSPROT-<br>ID:Q13829 TUMOR NECROSIS<br>FACTOR, ALPHA-INDUCED<br>PROTEIN 1, ENDOTHELIAL (B12<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 316 aa. | 1.70E-51  | 16 |





|     |            |      |   |   |     |  |  |  |                      |                      |   |           |               |
|-----|------------|------|---|---|-----|--|--|--|----------------------|----------------------|---|-----------|---------------|
| 144 | cg43917396 | 915  | TAGGGGCTGAA<br>ACGCAGTCGGG<br>GCC[G/gap]GGC<br>ACTGCCCAGGA<br>AGGGACTCCGG   | G | gap |  |  |  | SILENT-<br>NONCODING | transcript<br>factor | Human Gene Similar to<br>TREMBLNEW-ID:G2920821<br>TRANSCRIPTION FACTOR T-BOX 5<br>HOMO SAPIENS (HUMAN), 518 aa.   | 6.90E-68  |               |
| 145 | cg43949162 | 510  | TAGACAATACCA<br>TCTCTAGGAACA<br>C[A/G]CTGTCAC<br>TCACACATGGAT<br>GTGTTG     | A | G   |  |  |  | SILENT-<br>NONCODING | transferase          | Human Gene Homologous to<br>TREMBLNEW-ID:G2738933<br>GLUTATHIONE TRANSFERASE (EC<br>2.5.1.18) - HOMO SAPIENS<br>(HUMAN), 222 aa.  | 1.30E-115 | 6             |
| 146 | cg41653463 | 2407 | TGTGCGTGCGT<br>GTGTGTGTGTG<br>TGT[G/gap]TGTA<br>TCGTGTGTGTGT<br>GTTTTGTTT   | G | gap |  |  |  | SILENT-<br>NONCODING | transport            | Human Gene SWISSPROT-<br>ID:P31641 SODIUM- AND<br>CHLORIDE-DEPENDENT TAURINE<br>TRANSPORTER - HOMO SAPIENS<br>(HUMAN), 620 aa.  | 0.00E+00  | 3 (3p25)      |
| 147 | cg41653463 | 2408 | TGTGCGTGCGTG<br>TGTTGTGTGTGT<br>GTGT[G/gap]GTAT<br>CGTGTGTGTGT<br>GTTTTGTTT | T | gap |  |  |  | SILENT-<br>NONCODING | transport            | Human Gene SWISSPROT-<br>ID:P31641 SODIUM- AND<br>CHLORIDE-DEPENDENT TAURINE<br>TRANSPORTER - HOMO SAPIENS<br>(HUMAN), 620 aa.  | 0.00E+00  | 3 (3p25)      |
| 148 | cg43285429 | 388  | CCCAGTCAAGA<br>TAAGGAGGATC<br>CCA[G/A]CAGCT<br>CCCCTCCGAGG<br>TTGGGCTCT     | G | A   |  |  |  | SILENT-<br>NONCODING | transport            | Human Gene SWISSNEW-ID:P02730<br>BAND 3 ANION TRANSPORT<br>PROTEIN (ANION EXCHANGE<br>PROTEIN 1) (AE 1) - HOMO<br>SAPIENS (HUMAN), 911<br>aa.lpcis:SWISSPROT-ID:P02730<br>BAND 3 ANION TRANSPORT<br>PROTEIN (ANION EXCHANGE<br>PROTEIN 1) (AE 1) - HOMO<br>SAPIENS (HUMAN), 911 aa. | 0.00E+00  | 17<br>(17q21) |
| 149 | cg43918636 | 3322 | AGCAGCAGCTG<br>TTGGAGTAGAA<br>CCG[C/A]GTCCA<br>GGCGCGGACCA<br>TC TTCATCG    | C | A   |  |  |  | SILENT-<br>NONCODING | transport            | Human Gene Similar to SWISSPROT-<br>ID:Q15012 GOLGI 4-<br>TRANSMEMBRANE SPANNING<br>TRANSPORTER MTP (KIAA0108) -<br>HOMO SAPIENS (HUMAN), 233 aa.   | 5.40E-52  |               |

|     |            |      |  |     |     |  |  |  |                      |                  |   |           |    |
|-----|------------|------|--|-----|-----|--|--|--|----------------------|------------------|---|-----------|----|
| 150 | cg44005525 | 721  | TAAGCAGCTCTC<br>TTCTGTGACAGA<br>C[A]gapJAATCAT<br>GTAAGAAGCTGT<br>GAAACCCC | A   | gap |  |  |  | SILENT-<br>NONCODING | ubiquitin        | Human Gene Homologous to<br>SWISSPROT-ID:P51965 UBIQUITIN-<br>CONJUGATING ENZYME E2-21 KD<br>UBCH6 (EC 6.3.2.19) (UBIQUITIN-<br>PROTEIN LIGASE) (UBIQUITIN<br>CARRIER PROTEIN) - HOMO<br>SAPIENS (HUMAN), 193 aa. | 3.30E-101 |    |
| 151 | cg44005525 | 743  | GACAAATCATGT<br>AAGAACTGTGAA<br>A[C/A]CCAGTT<br>TATGTAGCGTAT<br>CTCTTG     | C   | A   |  |  |  | SILENT-<br>NONCODING | ubiquitin        | Human Gene Homologous to<br>SWISSPROT-ID:P51965 UBIQUITIN-<br>CONJUGATING ENZYME E2-21 KD<br>UBCH6 (EC 6.3.2.19) (UBIQUITIN-<br>PROTEIN LIGASE) (UBIQUITIN<br>CARRIER PROTEIN) - HOMO<br>SAPIENS (HUMAN), 193 aa. | 3.30E-101 |    |
| 152 | cg40986905 | 3075 | ATTTTATAGTAG<br>GACGGGGTTTC<br>AC[C/T]GTGTTA<br>GCCAGGATGGT<br>CTCGATCT    | C   | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14162 KIAA0149 PROTEIN -<br>HOMO SAPIENS (HUMAN), 830 aa.  | 0.00E+00  |    |
| 153 | cg43303871 | 1999 | AATAAGGGGAGA<br>ACTACTATTTTT<br>TT[gap/T]AAGAT<br>CTCAAAATAATT<br>AATAATAA | gap | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA25444 KIAA0518 PROTEIN -<br>HOMO SAPIENS (HUMAN), 650 aa<br>(fragment).   | 0.00E+00  |    |
| 154 | cg43303871 | 1999 | AATAAGGGGAGA<br>ACTACTATTTTT<br>TT[gap/T]AAGAT<br>CTCAAAATAATT<br>AATAATAA | gap | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA25444 KIAA0518 PROTEIN -<br>HOMO SAPIENS (HUMAN), 650 aa<br>(fragment).   | 0.00E+00  |    |
| 155 | cg43918386 | 3972 | CTTCTACCCCAT<br>GGGTAAATGTAT<br>TT[C]ACATATTA<br>CCAAGAGAAGA<br>AGCACA     | T   | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14511 ENHANCER OF<br>FILAMENTATION 1 - HOMO SAPIENS<br>(HUMAN), 834 aa.  | 0.00E+00  | 6  |
| 156 | cg43923712 | 501  | AGGAATCCTGG<br>ACAGGAGTTTTTC<br>TG[C/T]AGAGGC<br>GTTTAAACCCCT<br>ACCGAAT   | C   | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q12996 CLEAVAGE<br>STIMULATION FACTOR 77KDA<br>SUBUNIT - HOMO SAPIENS<br>(HUMAN), 717 aa.   | 0.00E+00  | 11 |

|     |            |       |  |   |     |  |  |  |                      |                  |   |          |                     |
|-----|------------|-------|--|---|-----|--|--|--|----------------------|------------------|---|----------|---------------------|
| 157 | cg43936083 | 189   | GCTAACTGGTG<br>ACAGTTATAAAA<br>AC[A/G]CAAAAA<br>GGAGCCTGGGA<br>AACAGCAA  | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O15089 KIAA0385 - HOMO<br>SAPIENS (HUMAN), 1370 aa.   | 0.00E+00 |                     |
| 158 | cg43936393 | 382   | AAAAACAAGTTT<br>CAGTAAAAA<br>A[A/gap]ACTAAA<br>ACAAACACTGAA<br>GTAGAGT   | A | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD22032 THYROID<br>HORMONE RECEPTOR-<br>ASSOCIATED PROTEIN COMPLEX<br>COMPONENT TRAP240 - HOMO<br>SAPIENS (HUMAN), 2174 aa. | 0.00E+00 | 17                  |
| 159 | cg43936393 | 383   | AAAAACAAGTTTC<br>AGTAAAAA<br>A[A/gap]CTAAAA<br>CAAACACTGAA<br>GTAGAGTT   | A | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD22032 THYROID<br>HORMONE RECEPTOR-<br>ASSOCIATED PROTEIN COMPLEX<br>COMPONENT TRAP240 - HOMO<br>SAPIENS (HUMAN), 2174 aa. | 0.00E+00 | 17                  |
| 160 | cg43940465 | 304   | ACTGTATTATTT<br>ATTACATGGGC<br>T[G/A]AAAGCAA<br>AGAAAAATGAGT<br>CCCTTC   | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O60300 KIAA0553 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1095 aa<br>(fragment).   | 0.00E+00 |                     |
| 161 | cg43940880 | 10186 | TAGTTTGTAAAG<br>ACTGTACAAAA<br>A[A/gap]TGCTTC<br>TGGAGATTTCCT<br>TGGCAGA | A | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P53794 SODIUM/MYO-<br>INOSITOL COTRANSPORTER<br>(NA(+)/MYO-INOSITOL<br>COTRANSPORTER) - Homo sapiens<br>(Human), 718 aa.     | 0.00E+00 | 21                  |
| 162 | cg43950657 | 1956  | TTTGGGATCCTG<br>ATCAATTCTTTC<br>T[G/A]ATGTTGTT<br>GAAAATGACAAA<br>GTTGG  | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q13009 T-LYMPHOMA<br>INVASION AND METASTASIS<br>INDUCING PROTEIN 1 (TIAM1<br>PROTEIN) - Homo sapiens (Human),<br>1591 aa.     | 0.00E+00 | 21<br>(21q22.1<br>) |

|     |            |      |   |   |     |  |  |  |                      |                  |  |          |                     |
|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|--|----------|---------------------|
| 163 | cg43950657 | 2033 | CAGCTGCCAAA<br>ACCGTGTGTGC<br>AAG[A/G]GCGCG<br>ACCTAAGGGGA<br>CATTCTTGT   | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q13009 T-LYMPHOMA<br>INVASION AND METASTASIS<br>INDUCING PROTEIN 1 (TIAM1<br>PROTEIN) - Homo sapiens (Human),<br>1591 aa.          | 0.00E+00 | 21<br>(21q22.1<br>) |
| 164 | cg43973740 | 485  | TGAAGCAAAACAA<br>ACAAACAAAAA<br>A[A/gap]GGAGAG<br>CTTCATTAGTAG<br>CCAAGAT | A | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q61123 MATERNAL<br>EMBRYONIC MESSAGE 3 (MEM3) -<br>MUS MUSCULUS (MOUSE), 754 aa.   | 0.00E+00 | 16<br>(12q12)       |
| 165 | cg43980521 | 1011 | GCGCATGGGTC<br>CCTCCAGGAAG<br>GCT[T/G]GGTTA<br>GAGTCCCAGGG<br>TGGTCCCCA   | T | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA20795 KIAA0337 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1510 aa.   | 0.00E+00 | 11                  |
| 166 | cg43980521 | 551  | CCCTCAGCTTTG<br>GGGGTCCTTC<br>CT[G/A]AAGGGG<br>CTTCCCTTGCA<br>GAAGGGG     | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA20795 KIAA0337 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1510 aa.   | 0.00E+00 | 11                  |
| 167 | cg43980521 | 873  | AGCATCTTGATC<br>TAGAGGACTGA<br>GG[G/A]CAGCCC<br>CATCAGGCTGG<br>GGCCCTGG   | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA20795 KIAA0337 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1510 aa.   | 0        | 11                  |
| 168 | cg44019839 | 3287 | AGCTACACAGA<br>GGAATAACTTA<br>GGT[C/J]ACTTTCT<br>GTTTTTTAAAA<br>AAAATA    | T | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:Q99743 NEURONAL PAS<br>DOMAIN PROTEIN 2 (NEURONAL<br>PAS2) (MEMBER OF PAS PROTEIN<br>4) (MOP4) - Homo sapiens (Human),<br>824 aa. | 0        |                     |

|     |            |      |  |   |   |  |  |  |                      |                  |  |          |   |
|-----|------------|------|--|---|---|--|--|--|----------------------|------------------|--|----------|---|
| 169 | cg44021891 | 787  | AGAAGACCTGG<br>CTTCTTACAAC<br>AG[G/A]GACAGG<br>CTGGTGGCTGG<br>GGCTAGAG   | G | A |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q92560 BRCA1 ASSOCIATED<br>PROTEIN 1 (MYELOBLAST<br>KIAA0272) - HOMO SAPIENS<br>(HUMAN), 729 aa. | 0        | 3 |
| 170 | cg44021891 | 869  | GCCCCCAGCTA<br>GGACCCTGTAG<br>TTG[G/A]GACCG<br>TGGCATGATACA<br>AGGACCTG  | G | A |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q92560 BRCA1 ASSOCIATED<br>PROTEIN 1 (MYELOBLAST<br>KIAA0272) - HOMO SAPIENS<br>(HUMAN), 729 aa. | 0        | 3 |
| 171 | cg44921773 | 2876 | TTCTGAGACAG<br>GGTCTTGCTCT<br>GTC[G/A]CCCCAG<br>GCTGGAGTGCA<br>ATGGCACGA | G | A |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13471 REPLICATION<br>CONTROL PROTEIN 1 - HOMO<br>SAPIENS (HUMAN), 861 aa.                       | 0        | 1 |
| 172 | cg44921773 | 2955 | GGGCTCAAGTG<br>ATCCTCCACCT<br>CA[A/G]CCTCCC<br>GAGTAGCTGAG<br>ACTACAGG   | A | G |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13471 REPLICATION<br>CONTROL PROTEIN 1 - HOMO<br>SAPIENS (HUMAN), 861 aa.                       | 0        | 1 |
| 173 | cg43961485 | 650  | GGTCTCCTCAG<br>TGGTCTATTTTA<br>GG[T/G]GTGGTT<br>TTTTTTTTTTTT<br>TTACTG   | T | G |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O60398 TXBP151 - HOMO<br>SAPIENS (HUMAN), 563 aa.  | 1.5E-303 | 7 |
| 174 | cg43985955 | 2111 | GAGCACAGATA<br>CAGTTTATGTAA<br>CTT[A/G]ATGGA<br>AGAAAATGGAAT<br>TACTCCA  | T | A |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13492 CALM (TYPE I CALM<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 652 aa.                          | 2.7E-299 |   |
| 175 | cg44916647 | 1142 | GCTCAGCAGCC<br>CCTAGGAAGTTA<br>AG[C/T]GAGAGC<br>TACAGGGCAGG<br>GGGGCTCC  | C | T |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75057 KIAA0469 PROTEIN -<br>HOMO SAPIENS (HUMAN), 539 aa.                                       | 4.3E-299 | 1 |

|     |            |      |  |   |     |  |  |  |                      |                  |   |          |    |
|-----|------------|------|--|---|-----|--|--|--|----------------------|------------------|---|----------|----|
| 176 | cg44916647 | 494  | TCTGTACATGTA<br>ACATGTGGCCA<br>TG[C/gap]CCAGG<br>CATCCAGCAT<br>CTATCCTGA | C | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75057 KIAA0469 PROTEIN -<br>HOMO SAPIENS (HUMAN), 539 aa.  | 4.3E-299 | 1  |
| 177 | cg44021459 | 2082 | GGTCACTGTTTC<br>CTCGGCATCGT<br>GC[T/C]GCCCTGG<br>AGAGAACTCCC<br>GACCGGGA | T | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAC16046 FIP2 - HOMO<br>SAPIENS (HUMAN), 577 aa.   | 1E-297   |    |
| 178 | cg43926814 | 372  | TAGAATTTTCTA<br>TCCCCCCCCATT<br>T[C/T]TCCAGTAA<br>TAAAAAGTAGTG<br>CTGGG  | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q13573 NUCLEAR PROTEIN<br>SKIP (SNW1 PROTEIN) (NUCLEAR<br>RECEPTOR COACTIVATOR NCOA-<br>62) - Homo sapiens (Human), 536 aa. | 5E-289   | 14 |
| 179 | cg43926814 | 412  | GTAGTGCTGGG<br>ATCTGGCACCC<br>AGA[T/C]TTGGTT<br>TTTATCCTGACC<br>ATTACA   | T | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q13573 NUCLEAR PROTEIN<br>SKIP (SNW1 PROTEIN) (NUCLEAR<br>RECEPTOR COACTIVATOR NCOA-<br>62) - Homo sapiens (Human), 536 aa. | 5E-289   | 14 |
| 180 | cg43931431 | 1415 | AGCCATGTACG<br>TGAAATTGCTTG<br>GG[A/T]ACCTGA<br>ACTCCCGCTGG<br>AATTCTA   | A | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:Q14154 HYPOTHETICAL<br>PROTEIN KIAA0141 - Homo sapiens<br>(Human), 515 aa.   | 7.2E-281 | 5  |
| 181 | cg44031765 | 277  | ATGCACCTGGC<br>CCACATGGCTG<br>GGC[G/A]CTGCA<br>GCCTGCACCTCC<br>ACTTCCAGG | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14776 LZTR-1 - HOMO<br>SAPIENS (HUMAN), 552 aa.  | 4.6E-279 | 22 |
| 182 | cg44031765 | 4030 | CATCTTTATAGG<br>CCACCACTGTG<br>TG[C/T]TTGCTG<br>CGCCGGGCACC<br>CACGAACT  | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14776 LZTR-1 - HOMO<br>SAPIENS (HUMAN), 552 aa.  | 4.6E-279 | 22 |

|     |            |      |  |   |     |  |  |                      |                  |  |           |    |
|-----|------------|------|--|---|-----|--|--|----------------------|------------------|--|-----------|----|
| 183 | cg43970492 | 331  | TGCTTTGTTGCT<br>TCAAGATGCATG<br>C[A/C]CATCCTG<br>GCTTTAGTGTC<br>AAGTAT     | A | C   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:P78395 PREFERENTIALLY<br>EXPRESSED ANTIGEN OF<br>MELANOMA - HOMO SAPIENS<br>(HUMAN), 509 aa. | 3.60E-270 | 22 |
| 184 | cg42847874 | 1118 | ACAAAATTAGC<br>CGGGCATGGTG<br>GC[G/A]CAGCC<br>TGAGTCCCAG<br>CTACTTAG       | G | A   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA34492 KIAA0772 PROTEIN<br>HOMO SAPIENS (HUMAN), 468 aa.                                  | 6.30E-258 | 20 |
| 185 | cg43951020 | 534  | GAGTGCAGTG<br>CTCACTGCAAC<br>CTC[C/T]GCCCTC<br>CCAGGTTCAAG<br>CAATTCCTCC   | C | T   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O76021 PBK1 PROTEIN -<br>HOMO SAPIENS (HUMAN), 516 aa.                                       | 6.60E-255 |    |
| 186 | cg43951020 | 552  | CAACCTCCGCC<br>TCCCAGGTTCAA<br>GC[A/G]ATTCTC<br>CTGCCTCAGCC<br>TCCCTAGT    | A | G   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O76021 PBK1 PROTEIN -<br>HOMO SAPIENS (HUMAN), 516 aa.                                       | 6.60E-255 |    |
| 187 | cg43971614 | 2720 | ACCAATTGCTTG<br>GTCAATTCAACC<br>TG[A/J]GGGGAA<br>AAGAGTCAAATA<br>TGTCCTA   | G | A   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13283 GAP SH3 BINDING<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 466 aa.                         | 5.30E-253 | 5  |
| 188 | cg43971614 | 2802 | CTCTGCACCCAC<br>AGCACCGAGGA<br>TAG[T/C]ACAAA<br>CCCCTCACGCG<br>TCTGCGTCC   | T | C   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13283 GAP SH3 BINDING<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 466 aa.                         | 5.30E-253 | 5  |
| 189 | cg43962954 | 192  | CGGGCTCCCCA<br>TGCAGCCCTAG<br>AGA[C/gap]GGG<br>AGAAAGTCCAGT<br>GTGCTGTTCCA | C | gap |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75455 HERPESVIRUS<br>ENTRY PROTEIN B - HOMO<br>SAPIENS (HUMAN), 479 aa.                     | 4.80E-252 | 19 |

|     |            |      |   |   |     |  |  |  |                      |                  |   |           |    |
|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|---|-----------|----|
| 190 | cg43917689 | 1684 | AGGCAACACCT<br>GTGAGGAAGG<br>GCACTTGGGGC<br>AAAAGCTCACCT<br>CAGAAAGTG     | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q92551 MYELOBLAST<br>KIAA0263 - HOMO SAPIENS<br>(HUMAN), 441 aa.  | 3.50E-240 | 3  |
| 191 | cg43917685 | 2176 | TCAGATGACTTT<br>ACAACCAAGG<br>AGT/CIACACAG<br>GGCAACAACAA<br>ATTAGAGG     | T | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAC97961 S164 - HOMO<br>SAPIENS (HUMAN), 735 aa<br>(fragment).   | 2.50E-230 | 14 |
| 192 | cg43287642 | 307  | GCAACTTATTT<br>AAAACCCAAAG<br>GA[G/A]AAAGGA<br>TGGTACTACCAT<br>AAATCAC    | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD20347 NEBULIN - HOMO<br>SAPIENS (HUMAN), 977 aa<br>(fragment).  | 3.50E-224 |    |
| 193 | cg43986954 | 1072 | AGTGGAAACATT<br>TTTGTTCATTT<br>CTT/CJAGGAATTT<br>TCTCTTGGGA<br>AAGTCG     | T | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAC68871 METHYL-CPG<br>BINDING PROTEIN MBD2 - HOMO<br>SAPIENS (HUMAN), 411 aa.                             | 9.40E-224 | 18 |
| 194 | cg42882543 | 3078 | TCCCGAGTAGC<br>TGGGATTACAG<br>GCA[T/C]GCGCC<br>ACCACGCCCCAG<br>CTAATTTTT  | T | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75177 KIAA0693 PROTEIN -<br>HOMO SAPIENS (HUMAN), 404 aa<br>(fragment).                                    | 2.30E-220 |    |
| 195 | cg43062833 | 1567 | TGAAAAGTATTA<br>TGGAAATCACTG<br>C[A/T]GCACAGG<br>AAAAGTAATTCA<br>GATGTT   | A | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q93088 BETAINE--<br>HOMOCYSTEINE S-<br>METHYLTRANSFERASE (EC<br>2.1.1.5) - Homo sapiens (Human),<br>406 aa. | 2.10E-219 | 5  |
| 196 | cg43959148 | 342  | AGACTAGTGTG<br>GGCCTTGGGCC<br>CCC[C/gap]TCAT<br>TTTGACATCCTT<br>CCAGATGGT | C | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75955 FLOTILLIN-1 - HOMO<br>SAPIENS (HUMAN), 427 aa.   | 1.40E-215 | 6  |



|     |            |      |   |   |     |  |  |  |                      |                  |   |           |               |
|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|---|-----------|---------------|
| 197 | cg43950766 | 385  | GTTCACATTTAG<br>TGAACCTGCATT<br>TTC/gapJATGGGG<br>GGGGGGGGGG<br>TACACAGTA | C | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD44491 PTD004 - HOMO<br>SAPIENS (HUMAN), 396 aa.   | 5.30E-214 | 22            |
| 198 | cg43958860 | 1340 | TCTGTCTTTTAT<br>TTAACAAAAAT<br>GTC/CJAATTAAT<br>GTAAACTTGGAA<br>TCAAG     | T | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P48745 NOV PROTEIN<br>HOMOLOG PRECURSOR (NOVH) -<br>Homo sapiens (Human), 357 aa.                          | 6.00E-206 | 8<br>(8q24.1) |
| 199 | cg43968205 | 1516 | CTATAGCAGAG<br>GGGGTTATGGG<br>GGC[G/A]GGAGG<br>GTAGACTGACAT<br>ACAGAAAGT  | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:CAB46373 HYPOTHETICAL<br>71.0 KD PROTEIN - HOMO SAPIENS<br>(HUMAN), 653 aa (fragment).                     | 6.90E-206 |               |
| 200 | cg43950996 | 825  | ACGCCAGTCCA<br>GAAAGAAGGTG<br>CTG[G/A]AGCCC<br>CTGCTCTGTCCT<br>CTCCATCA   | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:P78545 ESE-1B - HOMO<br>SAPIENS (HUMAN), 371 aa.  | 6.20E-204 | 1             |
| 201 | cg44924222 | 1787 | TAAGGGTGAGC<br>AGCAGCAGGAG<br>CGC[A/T]TTGAA<br>GAAGAAAGTAGA<br>AGGGGATGT  | A | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:P27539 EMBRYONIC<br>GROWTH/DIFFERENTIATION<br>FACTOR 1 PRECURSOR (GDF-1) -<br>Homo sapiens (Human), 372 aa. | 2.7E-203  |               |
| 202 | cg44924222 | 1834 | ATGTCAGGCAC<br>CGTGCGCAGAC<br>TGC[A/G]GTGAC<br>TGGTGGCATAAC<br>AGGACCTTG  | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:P27539 EMBRYONIC<br>GROWTH/DIFFERENTIATION<br>FACTOR 1 PRECURSOR (GDF-1) -<br>Homo sapiens (Human), 372 aa. | 2.7E-203  |               |
| 203 | cg44924222 | 2073 | GTACCGGAAGG<br>CGTAGGAGGAG<br>ACG[A/G]TTGAGG<br>ATGAGAGTGAC<br>CACGTGGTG  | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:P27539 EMBRYONIC<br>GROWTH/DIFFERENTIATION<br>FACTOR 1 PRECURSOR (GDF-1) -<br>Homo sapiens (Human), 372 aa. | 2.7E-203  |               |

|     |            |      |  |     |   |  |  |                      |                  |   |          |   |
|-----|------------|------|--|-----|---|--|--|----------------------|------------------|---|----------|---|
| 204 | cg44916575 | 1943 | GAGGACAAAA<br>CAGAAAGCCCT<br>GTG[AT]GTGTG<br>GGAAAACTCCG<br>CTGCAGAGA      | A   | T |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q16842 BETA-GALACTOSIDE<br>ALPHA-2,3-SIALYLTRANSFERASE<br>(EC 2.4.99.4) (CMP-N-<br>ACETYLNEURAMINATE-BETA-<br>GALACTOSAMIDE-ALPHA-2,3-<br>SIALYL-TRANSFERASE) - HOMO<br>SAPIENS (HUMAN), 350 aa.  | 3.7E-197 |   |
| 205 | cg42650960 | 2321 | GGCTGGAGTGC<br>AGTGGCACGAT<br>CTC[G/A]GCTCA<br>CTGCAAGCCTC<br>CGCCTCCCG    | G   | A |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:Q10981 GALACTOSIDE 2-L-<br>FUCOSYLTRANSFERASE 2 (EC<br>2.4.1.69) (GDP-L-FUCOSE:BETA-D-<br>GALACTOSIDE 2-ALPHA-L-<br>FUCOSYLTRANSFERASE 2)<br>(ALPHA(1,2)FT 2)<br>(FUCOSYLTRANSFERASE 2)<br>(SECRETOR BLOOD GROUP<br>ALPHA-2-<br>FUCOSYLTRANSFERASE)<br>(SECRETOR FACTOR) (SE) (SE2) -<br>Homo sapiens (Human), 343 aa. | 2E-189   |   |
| 206 | cg43947129 | 2163 | CTGGGGGCGTC<br>CATGGTGC GGC<br>GGC[G/C]AGGGC<br>GGTGAGTCAGC<br>CAAGGAGGA   | G   | C |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P10658 PROBABLE<br>PHOSPHOSERINE<br>AMINOTRANSFERASE (EC 2.6.1.52)<br>(PSAT) (ENDOMETRIAL<br>PROGESTERONE-INDUCED<br>PROTEIN) (EPIP) - Oryctolagus<br>cuniculus (Rabbit), 370 aa.  | 3E-188   |   |
| 207 | cg43922383 | 199  | ATCTGAAAAATGG<br>TGTTGTGGCGTC<br>GC[G/A]CGCGCC<br>AGCTATCGTCA<br>GTGCCCTTT | G   | A |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q15435 YEAST SDS22<br>HOMOLOG - HOMO SAPIENS<br>(HUMAN), 360 aa.  | 7.3E-185 | 2 |
| 208 | cg43922383 | 222  | CGCGGCCAGC<br>TATCGTCAGTGC<br>CT[gap/G]TTATT<br>GCCATTGGGTTT<br>GTGACTGT   | gap | G |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q15435 YEAST SDS22<br>HOMOLOG - HOMO SAPIENS<br>(HUMAN), 360 aa.  | 7.3E-185 | 2 |

|     |            |      |  |   |     |  |  |  |                      |                  |  |           |    |
|-----|------------|------|--|---|-----|--|--|--|----------------------|------------------|--|-----------|----|
| 209 | cg43922383 | 239  | TCAGTGCCTTTA<br>TTGCCATTGGGT<br>TTT/gapGTGACT<br>GTTGATATAGTG<br>ACGACCT   | T | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q15435 YEAST SDS22<br>HOMOLOG - HOMO SAPIENS<br>(HUMAN), 360 aa.                                 | 7.3E-185  | 2  |
| 210 | cg43922383 | 250  | ATTGCCATTGG<br>GTTTGTGACTGT<br>TG/A/GJTATAGT<br>GACGACCTCAG<br>GAGCAACA    | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q15435 YEAST SDS22<br>HOMOLOG - HOMO SAPIENS<br>(HUMAN), 360 aa.                                 | 7.3E-185  | 2  |
| 211 | cg43922383 | 263  | TTGTGACTGTTG<br>ATATAGTGACGA<br>C[C/G]TCAGGAG<br>CAACAGGTGGG<br>TTAAAAA    | C | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q15435 YEAST SDS22<br>HOMOLOG - HOMO SAPIENS<br>(HUMAN), 360 aa.                                 | 7.3E-185  | 2  |
| 212 | cg43953935 | 458  | CTTTTAAATAA<br>ATGACTGCCGAG<br>TG/A/GJGTGTA<br>ATTCTGAGAAAA<br>TTACATT     | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD41634 LYOSOMAL<br>TRAFFICKING REGULATOR 2 -<br>MUS MUSCULUS (MOUSE), 703 aa<br>(fragment).   | 2.4E-177  | 13 |
| 213 | cg43933591 | 1167 | ACATTTTGAATT<br>TTAGCTTTTTTTT<br>[T/gap]GCCCTCTC<br>TACTGTGTCACT<br>AAATAT | T | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q18476 C35A5.8 -<br>CAENORHABDITIS ELEGANS, 1078<br>aa.  | 1.70E-176 | 8  |
| 214 | cg43949875 | 2329 | CTGAGTAGCTG<br>GGATTACAGGC<br>GTG[T/C]GCCAC<br>CATGCCCCAGCT<br>AATTTTTTG   | T | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD34394 NUCLEAR PORE<br>COMPLEX INTERACTING PROTEIN<br>NPIP - HOMO SAPIENS (HUMAN),<br>350 aa. | 6.60E-175 |    |
| 215 | cg43100840 | 1131 | GGACAGGGGTG<br>CAGCTGGCAGC<br>CGA[G/A]AAAGG<br>GGACCACCTCG<br>GAGGGCTGG    | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P49752 HYPOTHETICAL<br>PROTEIN ZAP113 - Homo sapiens<br>(Human), 309 aa (fragment).             | 3.20E-168 |    |

|     |            |      |   |   |     |  |  |  |                      |                  |   |           |    |
|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|---|-----------|----|
| 216 | cg43922270 | 2077 | TGTATATGTGTA<br>CGTAGGTAGAT<br>GT[G/A]TGCAGC<br>ATGCGGCAGGT<br>TTGCCAGG   | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:Q14140 HYPOTHETICAL<br>PROTEIN KIAA0127 - Homo sapiens<br>(Human), 314 aa.   | 1.30E-162 | 2  |
| 217 | cg43993462 | 1461 | CAGAATGAGCT<br>GCAGAGGTTTC<br>CTC[C/T]CTGCTT<br>TACAATCCCTTA<br>TTGAAGT   | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q63965 TRICARBOXYLATE<br>CARRIER - RATTUS NORVEGICUS<br>(RAT), 357 aa (fragment).   | 5.10E-161 | 5  |
| 218 | cg43993462 | 384  | TAAACATCTACA<br>GAGTTGAAACAT<br>A[A/C]TCTGTCAT<br>ATTAAATATATT<br>ATCTA   | A | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q63965 TRICARBOXYLATE<br>CARRIER - RATTUS NORVEGICUS<br>(RAT), 357 aa (fragment).   | 5.1E-161  | 5  |
| 219 | cg43993462 | 624  | TAGTCTCACTTC<br>TTACCAAAAAA<br>A[A/gap]CAATGA<br>ACTGGATTGAG<br>CCCACTCA  | A | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q63965 TRICARBOXYLATE<br>CARRIER - RATTUS NORVEGICUS<br>(RAT), 357 aa (fragment).   | 5.1E-161  | 5  |
| 220 | cg43329741 | 996  | GCAGTGCAGGA<br>GATGACAGAGT<br>GAG[G/A]AGGGC<br>CCAGAGCAGAA<br>TTCTGGCCC   | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD3906 FH1/FH2 DOMAIN-<br>CONTAINING PROTEIN FHOS -<br>HOMO SAPIENS (HUMAN), 1164 aa.   | 6.7E-159  |    |
| 221 | cg42910688 | 1687 | AAACAATTTTG<br>TTCAATGCCCCAC<br>C[G/A]AGACATA<br>TAGAATTGGGAA<br>CTGATA   | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P55040 GTP-BINDING<br>PROTEIN GEM (GTP-BINDING<br>MITOGEN-INDUCED T-CELL<br>PROTEIN) (RAS-LIKE PROTEIN KIR)<br>- Homo sapiens (Human), 296 aa. | 7.7E-158  | 8  |
| 222 | cg43967474 | 969  | TGCTGGGGACC<br>ATGGATGGGGA<br>GGA[G/gap]GGG<br>CACAGGGCCCA<br>GTGCAGATGAA | G | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA76848 KIAA1004 PROTEIN -<br>HOMO SAPIENS (HUMAN), 496 aa<br>(fragment).   | 1.70E-152 | 11 |

|     |            |      |   |   |     |  |  |  |                      |                  |   |           |   |
|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|---|-----------|---|
| 223 | cg43964140 | 160  | GCTGAGATCTTA<br>GGTCAAAAAGC<br>TAIC/TJAGAAAA<br>GAAATCACTTTG<br>AAAAACA   | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAC69899<br>SACM21 - MUS MUSCULUS<br>(MOUSE), 721 aa.                                     | 1.10E-150 | 6 |
| 224 | cg43990820 | 325  | CCGGTTTAAAAG<br>GAAAAGTAAAAA<br>AIC/AJAATCCAC<br>AGTTGAGCAGTT<br>GATGTG   | C | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q15024 MRNA<br>(HA0800) FOR ORF - HOMO<br>SAPIENS (HUMAN), 290 aa<br>(fragment).           | 3.30E-150 | 3 |
| 225 | cg43930377 | 682  | TCACAGCTGGA<br>TTGAAAGAGTAT<br>TT[G/A]GGAAT<br>GTGGCAATGTT<br>GTTTATAT    | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:CAB43230<br>HYPOTHETICAL 33.3 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 290 aa<br>(fragment). | 7.80E-149 | 4 |
| 226 | cg43969800 | 503  | GCAAGACGTGT<br>CAGGGGAACCA<br>AGG[C/T]TCAGA<br>TCATTCCCCCTT<br>CATCTACA   | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:P25686 DNAJ<br>PROTEIN HOMOLOG 1 (HSJ-1) -<br>Homo sapiens (Human), 351 aa.                | 1.20E-145 | 2 |
| 227 | cg43973724 | 2109 | TATAAGTGATG<br>CAATAGAAATTT<br>G[G/T]ATTTTGT<br>ATAGAAAATTTA<br>CCTTG     | G | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O75070 KIAA0483<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 299 aa (fragment).                   | 1.30E-141 | 1 |
| 228 | cg43258867 | 112  | GGCCCAGTCCT<br>GGGGCTCTGGG<br>AGG[C/gap]TCAC<br>GCTCCCTCCTC<br>AGGCTGGGGA | C | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q99773<br>HYPOTHETICAL 30.9 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 285 aa.                  | 2.60E-141 |   |
| 229 | cg42907867 | 792  | GACGATGTGGA<br>CGCTGGGAGGG<br>ATC[T/gap]TGGC<br>GTTGGTTTCTG<br>AAAGCCAGG  | T | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q99769<br>HYPOTHETICAL 26.4 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 255 aa.                  | 1.10E-140 | 1 |

|     |            |      |   |   |     |  |  |  |                      |                  |   |           |                     |
|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|---|-----------|---------------------|
| 230 | cg43920176 | 2819 | AAAGCTGCTTTG<br>TTAGGTTCCCTTA<br>T[G/T]TTTTATTA<br>ACTGTCITTTTCT<br>CAGTT | G | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAD28325<br>LUMAN2 - HOMO SAPIENS<br>(HUMAN), 272 aa.   | 1.40E-140 |                     |
| 231 | cg43920176 | 2909 | ATTTTGTCATTT<br>TTTACATCAACT<br>T[C/T]ATGGTCTT<br>GTTTTACATGG<br>TAATT    | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAD28325<br>LUMAN2 - HOMO SAPIENS<br>(HUMAN), 272 aa.   | 1.40E-140 |                     |
| 232 | cg43950100 | 856  | CAAAATTAAACA<br>ATTCACAAAATA<br>C[A/G]ACAGCTA<br>GAATTACAAAAT<br>CCATTC   | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O14681 PIG8 -<br>HOMO SAPIENS (HUMAN), 318 aa.   | 1.70E-139 | 11                  |
| 233 | cg43950100 | 952  | GGCACAGGGAG<br>AAAAACAAAGTG<br>TT[C/gap]CAATC<br>AGTCCAGGCAC<br>AGGGACTGG | C | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O14681 PIG8 -<br>HOMO SAPIENS (HUMAN), 318 aa.   | 1.70E-139 | 11                  |
| 234 | cg43950100 | 391  | ACATTGACCCCT<br>TCAGTTCCTATA<br>T[G/A]CAGCACCC<br>CAATATTCTTT<br>GAAATA   | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O14681 PIG8 -<br>HOMO SAPIENS (HUMAN), 318 aa.   | 1.70E-139 | 11                  |
| 235 | cg43950100 | 515  | CAGGTTTAGTGT<br>TGTTGTAGTGG<br>CA[C/T]TTGTCCA<br>GAATTGGTACCT<br>CCCCAT   | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O14681 PIG8 -<br>HOMO SAPIENS (HUMAN), 318 aa.   | 1.70E-139 | 11                  |
| 236 | cg43132640 | 1317 | CTCTATGAACTC<br>TGTTTCTTTTCT<br>A[A/gap]TGAGAT<br>ATTAAACCATGT<br>AAAGAAC | A | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:P11226<br>MANNOSE-BINDING PROTEIN C<br>PRECURSOR (MBP-C) (MBP1)<br>(MANNAN-BINDING PROTEIN)<br>(MANNOSE-BINDING LECTIN) -<br>Homo sapiens (Human), 248 aa. | 4.20E-134 | 10<br>(10q11.2<br>) |

|     |            |      |  |   |     |  |  |  |                      |                  |  |           |    |
|-----|------------|------|--|---|-----|--|--|--|----------------------|------------------|--|-----------|----|
| 237 | cg44938448 | 1310 | TGAAAGTTAGAGT<br>AGCTGCAAATCT<br>CT[ <i>gap</i> ]TAAGTA<br>TCAATGTAAAGA<br>AGCAGAT | T | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O75035 KIAA0447<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 254 aa.                                     | 4.80E-129 | 1  |
| 238 | cg44938448 | 511  | AATGCCACTTTC<br>AGATGGAAGGG<br>AA[ <i>gap</i> ]TGAGAT<br>GGAAACAACA<br>AAAAAGGA    | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O75035 KIAA0447<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 254 aa.                                     | 4.80E-129 | 1  |
| 239 | cg43949897 | 923  | AGCACTTTGGA<br>GCTGGCCTCGC<br>CCC[C/ <i>gap</i> ]TAGG<br>AGGAGAGGGTC<br>CCTCCTGGGT | C | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O60499 SYNTAXIN<br>10 - HOMO SAPIENS (HUMAN), 249<br>aa.  | 1.80E-126 | 19 |
| 240 | cg42549778 | 1067 | GGGGGTGCTCC<br>TGGAAGCCCCA<br>AGA[G/C]CATCC<br>AGGATTGCCTC<br>CCAGCTGCC            | G | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAD29690<br>PUTATIVE ZINC FINGER<br>TRANSCRIPTION FACTOR OVO1 -<br>MUS MUSCULUS (MOUSE), 267 aa. | 3.70E-126 |    |
| 241 | cg44028574 | 990  | CAGCTCCCAGC<br>TACCATGATGAG<br>CC[C/ <i>gap</i> ]TGGC<br>GGCTTGAGCAC<br>AGTGAGTGCT | C | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAD27724 CGI-<br>15 PROTEIN - HOMO SAPIENS<br>(HUMAN), 329 aa.                                   | 4.00E-122 | 20 |
| 242 | cg44035718 | 1088 | TCTCATCTAGTG<br>CTGAAGTCTGA<br>GG[G/A]CTCTGC<br>AGCATCAGACC<br>CACCTCTA            | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:BAA83010<br>KIAA1058 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1534 aa<br>(fragment).                   | 2.20E-121 | 2  |

|     |            |      |   |   |     |  |  |  |  |                      |                  |  |           |    |
|-----|------------|------|---|---|-----|--|--|--|--|----------------------|------------------|--|-----------|----|
| 243 | cg44035718 | 1172 | GAAGAGAAAGA<br>TAGGTTTAATTT<br>ATT/CJTGAAAGTT<br>TTCATGGTGTTA<br>ATAATT   | T | C   |  |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:BAA83010<br>KIAA1058 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1534 aa<br>(fragment). | 2.20E-121 | 2  |
| 244 | cg43963595 | 1212 | CCCCGCAGAC<br>AGAGCCCGGAG<br>GCTT/GJCTGG<br>TGCAGCGATGT<br>TTAATGGCA      | T | G   |  |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O75391 SPERM<br>ACROSOMAL PROTEIN - HOMO<br>SAPIENS (HUMAN), 293 aa.            | 8.50E-120 | 17 |
| 245 | cg43963595 | 1213 | CCCCGCAGACA<br>GAGCCCGGAGG<br>CTTT/GJCTGGT<br>GCAGCGATGTT<br>TAATGGCAA    | T | G   |  |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O75391 SPERM<br>ACROSOMAL PROTEIN - HOMO<br>SAPIENS (HUMAN), 293 aa.            | 8.50E-120 | 17 |
| 246 | cg43963595 | 1402 | ATGTTACAGTAT<br>GTACAAAGACCC<br>CTC[gap]CCCTC<br>GGGGGACGGG<br>GCGGACTCCG | C | gap |  |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O75391 SPERM<br>ACROSOMAL PROTEIN - HOMO<br>SAPIENS (HUMAN), 293 aa.            | 8.50E-120 |    |
| 247 | cg43992566 | 492  | AAATAGAGAAATC<br>CAGACCCTTCC<br>CA[G/A]ATAATTT<br>AAGAACTGAGTT<br>TTCCTC  | G | A   |  |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:O14530 PROTEIN<br>1-4 - Homo sapiens (Human), 226 aa.                           | 5.40E-118 |    |
| 248 | cg43992566 | 670  | ATTATAATCTGA<br>AGCAGAAAAAAA<br>A[A/gap]GACAAT<br>TTACAAAGAAAT<br>ATTGAGC | A | gap |  |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:O14530 PROTEIN<br>1-4 - Homo sapiens (Human), 226 aa.                           | 5.40E-118 |    |
| 249 | cg43067745 | 907  | TCCCTGCACGC<br>CTTTACGTCAGA<br>CT[G/A]TCACCA<br>CAAGAGCCTTG<br>AGTGTC     | G | A   |  |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O75839 TSC501<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 227 aa.                     | 6.90E-118 |    |



|     |            |      |  |   |     |  |  |  |                      |                  |  |           |    |
|-----|------------|------|--|---|-----|--|--|--|----------------------|------------------|--|-----------|----|
| 250 | cg42697161 | 552  | ACGTGGTGCTG<br>GTAGTGCTTGT<br>TG[AG]GTGTGA<br>ATTCTCTCTCAT<br>ACAAAAG    | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O15262 RING<br>FINGER PROTEIN - HOMO<br>SAPIENS (HUMAN), 247 aa.  | 1.00E-114 | 4  |
| 251 | cg43957889 | 1466 | GTGCAATGGCA<br>TGATCTCGGCT<br>CAC[C/T]GCAAC<br>CTGTGCCTCCC<br>GGGTTCAAG  | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O00577 COSMID<br>6E5 CDK4, SAS AND KIAA0167<br>GENES, COMPLETE CDS, AND OS9<br>- HOMO SAPIENS (HUMAN), 227 aa.  | 2.70E-111 | 12 |
| 252 | cg42397024 | 404  | AACGCGAGACA<br>AATTTTCAAAT<br>CA[C/A]TCTTTA<br>CTTCTCCAAGAT<br>CTTCGA    | C | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:O43583 DRP1<br>PROTEIN (DRP) - Homo sapiens<br>(Human), 243 aa.   | 4.30E-109 |    |
| 253 | cg43976566 | 711  | CTTTAATGAAAC<br>ACTTTGGATCGT<br>C[A/G]GTGCTGA<br>AGTGAAAAGAAT<br>GTGCTG  | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:BAA74894<br>KIAA0871 PROTEIN - HOMO<br>SAPIENS (HUMAN), 469 aa.  | 1.70E-107 | 4  |
| 254 | cg44001900 | 936  | GATGCTAAAAG<br>CTTCTGCGAAAT<br>GT[G/A]TTCACG<br>TTTAATGTTGGG<br>AAATCCC  | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:BAA83057<br>KIAA1105 PROTEIN - HOMO<br>SAPIENS (HUMAN), 730 aa<br>(fragment).  | 1.20E-104 |    |
| 255 | cg43954569 | 471  | TTCAGCCACAT<br>GACTCAGGGAC<br>AC[A/gap]CTCCC<br>CAGCGGTTGCT<br>GGAGGCACC | A | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:P78560 DEATH<br>DOMAIN CONTAINING PROTEIN<br>CRADD (CASPASE AND RIP<br>ADAPTATOR WITH DEATH<br>DOMAIN) (RIP ASSOCIATED<br>PROTEIN WITH A DEATH DOMAIN) -<br>Homo sapiens (Human), 199 aa. | 1.40E-101 | 12 |
| 256 | cg43925519 | 791  | AGTGGCCCTT<br>TCCCGCCCTGA<br>AGA[T/C]GTTTCA<br>CACGAAAAGGC<br>CGTTTGTT   | T | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P78317 ZINC FINGER<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 190 aa.  | 4.40E-100 | 4  |

|     |            |      |  |   |   |  |  |                      |                  |   |          |   |
|-----|------------|------|--|---|---|--|--|----------------------|------------------|---|----------|---|
| 257 | cg43145684 | 711  | TGGCAAACTG<br>CCAGCAGCGGT<br>TGC[CT]GAAAA<br>TGCTGGGTTGG<br>GTGCCTACT    | C | T |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA81668 DNA<br>POLYMERASE ETA - HOMO<br>SAPIENS (HUMAN), 713 aa.                                  | 2.90E-99 |   |
| 258 | cg43981803 | 626  | ACCAGCTCGGA<br>GAGGGCACTTG<br>AGA[G/T]GGTCT<br>ATGAACAAATCT<br>GTCTAAAA  | G | T |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q16635 TFAZZIN - Homo<br>sapiens (Human), 292 aa.   | 7.1E-97  | X |
| 259 | cg44006111 | 1906 | AGGCCTGATGC<br>ACATGTGCACA<br>GGT[A/G]CCTAC<br>ATGCTCTGTTCT<br>TGTCACAA  | A | G |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to REMTREMBL-<br>ACC:G1100182 T-CELL RECEPTOR<br>BETA - HOMO SAPIENS (HUMAN),<br>311 aa.                               | 3.8E-95  |   |
| 260 | cg44924968 | 1363 | TGGCCAGGGAC<br>CTGAGCCCCGAG<br>ACA[C/T]CCCTG<br>CATTGATCCAA<br>CCAGGTCA  | C | T |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD43192<br>WUGSC:H_DJ0726N20.1 PROTEIN -<br>HOMO SAPIENS (HUMAN), 191 aa<br>(fragment).           | 6.8E-95  | 7 |
| 261 | cg44924968 | 1364 | GGCCAGGGACC<br>TGAGCCCCGAGA<br>CAC[C/T]CCTGC<br>ATTGATCCCAAC<br>CAGGTCAG | C | T |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD43192<br>WUGSC:H_DJ0726N20.1 PROTEIN -<br>HOMO SAPIENS (HUMAN), 191 aa<br>(fragment).           | 6.80E-95 | 7 |
| 262 | cg43977021 | 1080 | TTGCATCTAAAG<br>TAATTCATTAAAT<br>GT[A]ACAGGAG<br>TAGATGAGGCC<br>TGGCACA  | T | A |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14206 ZAKI-4 MRNA IN<br>HUMAN SKIN FIBROBLAST,<br>COMPLETE CDS - HOMO SAPIENS<br>(HUMAN), 192 aa. | 9.20E-91 | 6 |
| 263 | cg43977021 | 1087 | TAAAGTAATTCA<br>TTAATGTACAGG<br>A[G/A]TAGATGA<br>GGCCTGGCACA<br>CATAGCA  | G | A |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14206 ZAKI-4 MRNA IN<br>HUMAN SKIN FIBROBLAST,<br>COMPLETE CDS - HOMO SAPIENS<br>(HUMAN), 192 aa. | 9.20E-91 | 6 |

|     |            |      |  |   |   |  |  |  |                      |                  |   |          |   |
|-----|------------|------|--|---|---|--|--|--|----------------------|------------------|---|----------|---|
| 264 | cg43977021 | 1098 | ATTAATGTACAG<br>GAGTAGATGAG<br>GC[C]/TJGGCAC<br>ACATAGCAGAA<br>GGTAATGG  | C | T |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14206 ZAKI-4 MRNA IN<br>HUMAN SKIN FIBROBLAST,<br>COMPLETE CDS - HOMO SAPIENS<br>(HUMAN), 192 aa. | 9.20E-91 | 6 |
| 265 | cg43977021 | 1107 | CAGGAGTAGAT<br>GAGGCCTGGCA<br>CAC[A]/GJTAGCA<br>GAAGGTAATGG<br>TTCTATAGG | A | G |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14206 ZAKI-4 MRNA IN<br>HUMAN SKIN FIBROBLAST,<br>COMPLETE CDS - HOMO SAPIENS<br>(HUMAN), 192 aa. | 9.20E-91 | 6 |
| 266 | cg43977021 | 1116 | ATGAGGCCTGG<br>CACACATAGCA<br>GAA[G]/AJGTAAT<br>GGTCTATAGGT<br>GTATCTTC  | G | A |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14206 ZAKI-4 MRNA IN<br>HUMAN SKIN FIBROBLAST,<br>COMPLETE CDS - HOMO SAPIENS<br>(HUMAN), 192 aa. | 9.20E-91 | 6 |
| 267 | cg43977021 | 1169 | TAATGCACCTTG<br>GGCTAGAGAAA<br>TA[G]/CJAAAAATC<br>ACACGTAACAAA<br>AACAAA | G | C |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14206 ZAKI-4 MRNA IN<br>HUMAN SKIN FIBROBLAST,<br>COMPLETE CDS - HOMO SAPIENS<br>(HUMAN), 192 aa. | 9.20E-91 | 6 |
| 268 | cg43999373 | 303  | CACAGAATTCAG<br>AACTTTTTCACC<br>C[G]/CJGAACTGG<br>AGAAGGAGCAC<br>TCCGTCA | G | C |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O88994 HYPOTHETICAL 38.2<br>KD PROTEIN - RATTUS<br>NORVEGICUS (RAT), 338 aa.                       | 1.50E-89 | 1 |
| 269 | cg43980889 | 915  | TTTGAGAGCTG<br>CAGCAGAAAGCG<br>GCT[G]/TJATCA<br>CAGACTGGATTT<br>AGTTATGA | G | T |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O00581 HYPOTHETICAL 20.5<br>KD PROTEIN - HOMO SAPIENS<br>(HUMAN), 176 aa.                          | 4.5E-89  |   |
| 270 | cg43980889 | 936  | GGCTGTATCAC<br>AGACTGGATTTA<br>GTT[G]/JATGATG<br>AAAATACTGGAC<br>TGTATTT | T | G |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O00581 HYPOTHETICAL 20.5<br>KD PROTEIN - HOMO SAPIENS<br>(HUMAN), 176 aa.                          | 4.5E-89  |   |

|     |            |     |   |   |     |  |  |  |                      |                  |  |          |    |
|-----|------------|-----|---|---|-----|--|--|--|----------------------|------------------|--|----------|----|
| 271 | cg44030196 | 611 | TAGATTGTTTCAG<br>TACTCAGCTCAC<br>C[A/gap]CCCAT<br>AGACCATTTCTC<br>CTCTGGC | A | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD40853<br>SIRTUIN TYPE 5 - HOMO SAPIENS<br>(HUMAN), 310 aa.   | 7.4E-89  |    |
| 272 | cg40336929 | 317 | GGCAACAAGTT<br>ACAGCGGGGG<br>AGAT[A]GTTCTT<br>TCTCTCACCTGC<br>CGGGGG      | T | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O73884 PUTATIVE<br>PHOSPHATASE - GALLUS GALLUS<br>(CHICKEN), 268 aa.                                      | 3.4E-84  |    |
| 273 | cg43920571 | 684 | AGAAGACAGCG<br>CGCAGAAATAG<br>TGC[G/A]GAGAG<br>AAATGACCAGTA<br>CTATTTAT   | G | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P34624 HYPOTHETICAL 63.5<br>KD PROTEIN ZK353.1 IN<br>CHROMOSOME III - Caenorhabditis<br>elegans, 548 aa. | 3.5E-82  | 10 |
| 274 | cg43958980 | 537 | TAAGATCCTCCA<br>TCCACCAAAAA<br>T[A/G]ACCCACA<br>ATGACTCCAAAT<br>CTTGTT    | A | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB43239<br>HYPOTHETICAL 41.6 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 383 aa<br>(fragment).                 | 4.50E-82 | 6  |
| 275 | cg43320682 | 512 | CATTGGCAACG<br>GCTGCCCACTA<br>GG[G/gap]CAC<br>TGCCACTTGCCT<br>GGCTCAAACT  | G | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB45773<br>HYPOTHETICAL 18.0 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 162 aa<br>(fragment).                 | 6.60E-81 |    |
| 276 | cg42708544 | 845 | CCAGGCTTGCC<br>TCTAGATTGGCT<br>GG[G/gap]CCAG<br>AATTCTGGGGT<br>CAGTCTGAA  | G | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O14684 PIG12 - HOMO<br>SAPIENS (HUMAN), 153 aa.   | 2.60E-79 |    |
| 277 | cg43949796 | 637 | GGGAAGTAAAA<br>TGAAGGAAGCA<br>GAC[C/T]TCTTG<br>CTCATCTTTCCA<br>AATGAAAT   | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q94547 RGA AND ATU<br>GENES, COMPLETE CDS -<br>DROSOPHILA MELANOGASTER<br>(FRUIT FLY), 579 aa.            | 1.20E-75 | 12 |

|     |            |      |   |     |     |  |  |  |                      |                  |   |          |    |
|-----|------------|------|---|-----|-----|--|--|--|----------------------|------------------|---|----------|----|
| 278 | cg43298234 | 843  | TAAGGCCAGAG<br>CTTGTGTGCTG<br>GGC[A/gap]CAGA<br>AATCACCTGCTG<br>CATCCTGTG | A   | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O60896 MRNA ENCODING<br>RAMP3 PRECURSOR - HOMO<br>SAPIENS (HUMAN), 148 aa.   | 1.30E-75 | 7  |
| 279 | cg43926358 | 607  | CAGTGATGTGC<br>TGGCCCTTTCA<br>GGG[A/C]CACAG<br>GCCCTTCAGC<br>TTCACCGGA    | A   | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O75272 R33729_1, PARTIAL<br>CDS - HOMO SAPIENS (HUMAN),<br>152 aa (fragment).  | 1.90E-74 | 19 |
| 280 | cg35060315 | 1328 | CCAAACTATCTC<br>ACCTACCCCTC<br>CC[T/C]AGGATC<br>CACTCTTTTGA<br>ATGACAA    | T   | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:P01225 FOLLITROPIN BETA<br>CHAIN PRECURSOR (FOLLICLE-<br>STIMULATING HORMONE) (FSH-B) -<br>Homo sapiens (Human), 129 aa. | 9.50E-73 | 11 |
| 281 | cg35060315 | 1540 | CTATTTTATCCA<br>TCCATGTTCTCC<br>C[A/gap]AATCTG<br>TGCTTTCTTTCA<br>ACAGGTT | A   | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:P01225 FOLLITROPIN BETA<br>CHAIN PRECURSOR (FOLLICLE-<br>STIMULATING HORMONE) (FSH-B) -<br>Homo sapiens (Human), 129 aa. | 9.50E-73 | 11 |
| 282 | cg35060315 | 1542 | TTTATCCATCC<br>ATGTTCTCCCAA<br>A[gap]/A/TCTGTG<br>CTTCTTTTCAAC<br>AGGTTAT | gap | A   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:P01225 FOLLITROPIN BETA<br>CHAIN PRECURSOR (FOLLICLE-<br>STIMULATING HORMONE) (FSH-B) -<br>Homo sapiens (Human), 129 aa. | 9.5E-73  | 11 |
| 283 | cg35060315 | 1557 | GTTCCTCCAAAT<br>CTGTGCTTTCTT<br>T[C/T]AACAGGTT<br>ATATATTAAAC<br>TATTT    | C   | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:P01225 FOLLITROPIN BETA<br>CHAIN PRECURSOR (FOLLICLE-<br>STIMULATING HORMONE) (FSH-B) -<br>Homo sapiens (Human), 129 aa. | 9.5E-73  | 11 |
| 284 | cg35060315 | 1562 | CCCAAATCTGTG<br>CTTGTCTTCAAC<br>A[G/C]GTTATATA<br>TTAAAACTATTT<br>CATGA   | G   | C   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:P01225 FOLLITROPIN BETA<br>CHAIN PRECURSOR (FOLLICLE-<br>STIMULATING HORMONE) (FSH-B) -<br>Homo sapiens (Human), 129 aa. | 9.5E-73  | 11 |

|     |            |      |   |   |     |  |  |  |                      |                  |  |         |    |
|-----|------------|------|---|---|-----|--|--|--|----------------------|------------------|--|---------|----|
| 285 | cg44126579 | 18   | TGTACAACTGAT<br>TAGAG[AGap]GT<br>TTTTTTTCTTT<br>TTCTTTTCAA                | A | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P90839 F16A11.1 -<br>CAENORHABDITIS ELEGANS, 673<br>aa.                               | 1.1E-71 | 16 |
| 286 | cg43951096 | 719  | CCTCTCCTCCAA<br>GAGTTGGTTCC<br>GC[AGap]AGAG<br>GTGGAAGAAC<br>TCTCAATAGT   | A | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q23382 ZK1058.4 -<br>CAENORHABDITIS ELEGANS, 442<br>aa.                               | 2E-71   | 17 |
| 287 | cg43951096 | 884  | CACAGCCATAAT<br>ATAGAGAACAG<br>AG[C]gapJTTCTC<br>CATGAACATCCA<br>CCAGGCTG | C | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q23382 ZK1058.4 -<br>CAENORHABDITIS ELEGANS, 442<br>aa.                               | 2E-71   | 17 |
| 288 | cg43960676 | 65   | AGCAGCCAGCT<br>TCATTGGCTGCA<br>AA[C]TJGCCTCT<br>CTCAGGTGAGT<br>CAAAGGAG   | C | T   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD43443 26S<br>PROTEASOME SUBUNIT P40.5 -<br>MUS MUSCULUS (MOUSE), 376 aa.           | 5.3E-69 |    |
| 289 | cg43323149 | 1101 | TCACCTCAGATG<br>AGTGTGGCTCC<br>CC[C]GJCGCTCC<br>CATACTGCAGC<br>CTGCCCCCT  | C | G   |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P50636 GAMETOGENESIS<br>EXPRESSED PROTEIN GEG-154 -<br>Mus musculus (Mouse), 429 aa. | 1E-68   | 1  |
| 290 | cg43969533 | 364  | AAGGGAAGCCT<br>ATCCTATTTTTT<br>TT[AGap]TCCCTT<br>GCGAAAACAGA<br>AGCCAAGT  | T | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD39844<br>HSPC028 - HOMO SAPIENS<br>(HUMAN), 419 aa.                                | 1.6E-67 | 7  |
| 291 | cg43969533 | 365  | AGGGAAGCCTA<br>TCCTATTTTTT<br>TT[AGap]CCCTTG<br>CGAAAACAGAA<br>GCCAAGTT   | T | gap |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD39844<br>HSPC028 - HOMO SAPIENS<br>(HUMAN), 419 aa.                                | 1.6E-67 | 7  |

|     |            |     |   |   |   |  |  |  |                      |                  |  |         |    |
|-----|------------|-----|---|---|---|--|--|--|----------------------|------------------|--|---------|----|
| 292 | cg39376027 | 601 | CCGGGGAGGTG<br>GTTCTGGTAATC<br>TG[GT]GGGGA<br>GCCGGGACAGG<br>CGCCCCGA   | G | T |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD39515<br>HERMES - MUS MUSCULUS<br>(MOUSE), 197 aa.         | 2.3E-66 |    |
| 293 | cg39376027 | 604 | GGGAGGTGGTT<br>CTGTAATCTG<br>GGG[GT]GGAGC<br>CGGACACGGCG<br>CCCCGAGTT   | G | T |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD39515<br>HERMES - MUS MUSCULUS<br>(MOUSE), 197 aa.         | 2.3E-66 |    |
| 294 | cg43976681 | 210 | CTCTCTCTTCGC<br>CGCCGACGCAG<br>AA[A]GIGGAGCT<br>GGGAGGAAAA<br>AGCTGCTG  | A | G |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD29427<br>MYOMEGALIN - RATTUS<br>NORVEGICUS (RAT), 2324 aa. | 4.3E-66 | 11 |
| 295 | cg43085556 | 131 | GTAAGGTAAAT<br>GTGAATCAATAT<br>G[T/C]TAGTTCT<br>GGCAATTATTC<br>TGCAAA   | T | C |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O60223 SSX3 - HOMO<br>SAPIENS (HUMAN), 188 aa.                | 8.8E-65 |    |
| 296 | cg43085556 | 149 | CAATATGTTAGT<br>TCTGGGCAATTA<br>TT[T/C]CTGCAAT<br>TCTGCCAGATAA<br>TTAAA | T | C |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O60223 SSX3 - HOMO<br>SAPIENS (HUMAN), 188 aa.                | 8.8E-65 |    |
| 297 | cg43085556 | 150 | AATATGTTAGTT<br>CTGGGCAATTAT<br>T[C/T]TGCAAAAT<br>CTGCCAGATAAT<br>TAAAG | C | T |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O60223 SSX3 - HOMO<br>SAPIENS (HUMAN), 188 aa.                | 8.8E-65 |    |
| 298 | cg43085556 | 30  | TTGTTGTTCTCA<br>AGCTTTTCGCCT<br>A[C/T]ATTTTGA<br>CTAACCCCTGCTT<br>ATTCC | C | T |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O60223 SSX3 - HOMO<br>SAPIENS (HUMAN), 188 aa.                | 8.8E-65 |    |

|     |            |      |  |     |     |  |  |                      |                  |   |         |    |
|-----|------------|------|--|-----|-----|--|--|----------------------|------------------|---|---------|----|
| 299 | cg43085556 | 45   | TTTTGCCTACA<br>TTTTAGACTAAC<br>C[C/T]TGCTTATT<br>CCTGTGAATCAA<br>GTGGT     | C   | T   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O60223 SSX3 - HOMO<br>SAPIENS (HUMAN), 188 aa.   | 8.8E-65 |    |
| 300 | cg43085556 | 65   | TAACCCCTGCTTA<br>TTCCTGTGAATC<br>A[A/C]GTGGTGA<br>TCTTCTGCAGCT<br>TGAAT    | A   | C   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O60223 SSX3 - HOMO<br>SAPIENS (HUMAN), 188 aa.   | 8.8E-65 |    |
| 301 | cg43920089 | 437  | GCATTTGCTGCT<br>TGTCCTTGATTT<br>T[G/A]TTTGGCT<br>CAATCCCTTCCT<br>GGCAGC    | G   | A   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O14716 DNAJ PROTEIN -<br>HOMO SAPIENS (HUMAN), 135 aa.   | 2E-63   |    |
| 302 | cg43950850 | 263  | AAACATGTTCCA<br>TCAAAATTCAGAA<br>A[C/gap]AGCAGG<br>TATCAGTGAAC<br>TGGAGCA  | C   | gap |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:O95298 NADH-UBIQUINONE<br>OXIDOREDUCTASE SUBUNIT<br>B14.5B (EC 1.6.5.3) (EC 1.6.99.3)<br>(COMPLEX I-B14.5B) (CI-B14.5B) -<br>Homo sapiens (Human), 119 aa. | 7.8E-62 | 11 |
| 303 | cg43950850 | 736  | AGGAAAACCCAC<br>GACGACCACTA<br>CCC[G/C]GGCCT<br>AAGCGGTCAGC<br>TTTCTCCTC   | G   | C   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:O95298 NADH-UBIQUINONE<br>OXIDOREDUCTASE SUBUNIT<br>B14.5B (EC 1.6.5.3) (EC 1.6.99.3)<br>(COMPLEX I-B14.5B) (CI-B14.5B) -<br>Homo sapiens (Human), 119 aa. | 7.8E-62 | 11 |
| 304 | cg44128084 | 1012 | CATCCGCGCTG<br>ACGGCAGTCAC<br>CGG[T/C]GAGAC<br>CGGCGCCGGAA<br>AGACCATGG    | T   | C   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O33196 HYPOTHETICAL 32.9<br>KD PROTEIN - MYCOBACTERIUM<br>TUBERCULOSIS, 307 aa.  | 1.7E-59 |    |
| 305 | cg43976473 | 984  | GACGCTCGCTG<br>TCCCCGAGGGC<br>CCG[gap/C]TGC<br>GCCGCCCTCGTG<br>GGTACGAATAC | gap | C   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O35946 HYPOTHETICAL 14.9<br>KD PROTEIN - RATTUS<br>NORVEGICUS (RAT), 137 aa.   | 3.5E-59 | 11 |



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|-----|------------|-----|--|---|---|--|--|--|----------------------|------------------|--|----------|----|
| 306 | cg44924858 | 546 | GCTTCTGTCAGAG<br>CGTTACTTTTCAC<br>C[G]AJTGCCTGC<br>TGTTCCACAGG<br>AAGAGT | G | A |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q12773 GUANINE<br>NUCLEOTIDE REGULATORY<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 460 aa.     | 4.3E-59  |    |
| 307 | cg44924858 | 558 | CGTTACTTTTCAC<br>CGTGCCTGCTG<br>TTT[C]CCACAG<br>GAAGAGTCTGT<br>CTGTTCCA  | T | C |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q12773 GUANINE<br>NUCLEOTIDE REGULATORY<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 460 aa.     | 4.3E-59  |    |
| 308 | cg44924858 | 755 | ACCCAGCTTG<br>CCCGGCAGCAC<br>ACA[A]GJAACGT<br>TTTCTTTGGCTT<br>GACGAATA   | A | G |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q12773 GUANINE<br>NUCLEOTIDE REGULATORY<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 460 aa.     | 4.30E-59 |    |
| 309 | cg43961591 | 222 | ACACCACTGGT<br>ACTCACACCCC<br>CTC[T/C]GGCTG<br>GGTCTCTGGT<br>GGCCCTGC    | T | C |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:O35414 STATHMIN-LIKE<br>PROTEIN B3 (RB3) - Rattus<br>norvegicus (Rat), 189 aa.           | 3.10E-58 |    |
| 310 | cg43924285 | 528 | CTGCATATGTTT<br>GCAGTTTTCAT<br>C[A/G]ACTTCTTC<br>ATAAACAAACAA<br>ACATT   | A | G |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD29804<br>F26H11.12 PROTEIN -<br>ARABIDOPSIS THALIANA (MOUSE-<br>EAR CRESS), 323 aa.    | 4.20E-57 | 15 |
| 311 | cg43924285 | 574 | ACATTTTCTAGA<br>AACCAAAATATG<br>T[A/G]GTGGCCC<br>AAAGGAGCTCTT<br>AAGCAA  | A | G |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD29804<br>F26H11.12 PROTEIN -<br>ARABIDOPSIS THALIANA (MOUSE-<br>EAR CRESS), 323 aa.    | 4.20E-57 | 15 |
| 312 | cg43958224 | 198 | GTTTGATCCTCA<br>GCCAGGACGCA<br>CA[G/A]GCCCTA<br>CAAGATCCCG<br>CCCTCCAA   | G | A |  |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB43298<br>HYPOTHETICAL 13.8 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 118 aa<br>(fragment). | 2.30E-53 | 19 |

|     |            |     |  |   |     |  |  |                      |                  |   |          |  |
|-----|------------|-----|--|---|-----|--|--|----------------------|------------------|---|----------|--|
| 313 | cg43971060 | 502 | AACGGCTTTAAA<br>CACAAAGCTCAG<br>GG[G]gapICTTG<br>GGGTTTATCCC<br>GAGGGCACAG | G | gap |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P31639 SODIUM/GLUCOSE<br>COTRANSPORTER 2<br>(NA(+)/GLUCOSE<br>COTRANSPORTER 2) (LOW<br>AFFINITY SODIUM-GLUCOSE<br>COTRANSPORTER) - Homo sapiens<br>(Human), 672 aa. | 4.20E-53 |  |
| 314 | cg44927952 | 342 | TATTTTTCATTG<br>TACTTATTATTC<br>A[T/C]TATACTTA<br>CTATATATATTT<br>AAAAAC   | T | C   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD34077 CGI-<br>82 PROTEIN - HOMO SAPIENS<br>(HUMAN), 318 aa.   | 4.80E-52 |  |
| 315 | cg19885484 | 77  | AAACAACAAAT<br>AACCACAAATAA<br>A[C/T]CAACTAAT<br>GCTACACAGAAT<br>GTGAT     | C | T   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O15019 KIAA0301 - HOMO<br>SAPIENS (HUMAN), 2047 aa<br>(fragment).  | 1.90E-51 |  |
| 316 | cg42307356 | 11  | CGGCCGCGG[C]<br>G/TJCGGAACGG<br>CGCCTCCCGCC<br>CCACCA                      | G | T   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O15121 PUTATIVE FATTY<br>ACID DESATURASE MLD - HOMO<br>SAPIENS (HUMAN), 323 aa.  | 2.60E-51 |  |
| 317 | cg44005017 | 947 | TGGGAGGCCTG<br>GTTGCCCTCC<br>CGG[C/T]GTGCT<br>GGGACACTCTG<br>GGTTCCTGC     | C | T   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB43363<br>HYPOTHETICAL 23.0 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 204 aa.  | 5.00E-51 |  |
| 318 | cg43329819 | 609 | TTGAGCTCTCCT<br>ACAAGCTGGAG<br>GC[A/C]AACAGT<br>CAGTGAGAGCG<br>GGGGGGCC    | A | C   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q92565 MYELOBLAST<br>KIAA0277 - HOMO SAPIENS<br>(HUMAN), 580 aa.   | 1.40E-50 |  |
| 319 | cg43329819 | 612 | AGCTCTCTTACA<br>AGCTGGAGGCA<br>AA[C/T]AGTCAG<br>TGAGAGCGGG<br>GGGCCAGT     | C | T   |  |  | SILENT-<br>NONCODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q92565 MYELOBLAST<br>KIAA0277 - HOMO SAPIENS<br>(HUMAN), 580 aa.   | 1.40E-50 |  |



|     |            |      |   |   |   |     |     |                   |                           |   |           |    |
|-----|------------|------|---|---|---|-----|-----|-------------------|---------------------------|---|-----------|----|
| 326 | cg43930957 | 1287 | AAATATAAACTC<br>TTTTGAAAGTTG<br>T[G]TGGTCAGC<br>TGACCAGGTAG<br>AGGATTC  | G | T | Val | Val | SILENT-<br>CODING | apoptosi<br>s             | Human Gene Homologous to<br>SPTREMBL-ID:Q62627 CLONE PAR-<br>4 INDUCED BY EFFECTORS OF<br>APOPTOSIS - RATTUS<br>NORVEGICUS (RAT), 332 aa.   | 1.6E-117  |    |
| 327 | cg43300636 | 413  | CAAGGCGGCA<br>AAGATGGGAC<br>CAG[C]TACCAC<br>AGCGCCACGC<br>CCACCTCCG     | C | T | Val | Val | SILENT-<br>CODING | ATPase_<br>associat<br>ed | Human Gene SPTREMBL-ID:Q29466<br>VACUOLAR H+-ATPASE SUBUNIT<br>(EC 3.6.1.34) (H+)-TRANSPORTING<br>ATP SYNTHASE) (H+)-<br>TRANSPORTING ATPASE)<br>(MITOCHONDRIAL ATPASE)<br>(CHLOROPLAST ATPASE)<br>(COUPLING FACTORS (F(O), F(1)<br>AND CF(1))) - BOS TAURUS<br>(BOVINE), 838 aa. | 1.7E-175  |    |
| 328 | cg43967912 | 749  | CATTCTCTCTCC<br>AAAATTTCTCAG<br>A[T]CJTGTGCA<br>CAGGACTCCATT<br>CCAACC  | T | C | Lys | Lys | SILENT-<br>CODING | ATPase_<br>associat<br>ed | Human Gene Homologous to<br>SPTREMBL-ID:Q22494 SIMILAR<br>TOS. CEREBISIAE VACUOLAR H(+)-<br>ATPASE 54 KD SUBUNIT -<br>CAENORHABDITIS ELEGANS, 470<br>aa.  | 5.6E-108  | 8  |
| 329 | cg43967912 | 761  | AAATTTCTCAG<br>ATTTGTGCACAG<br>G[A]GJCTCCATT<br>CCAACCTTCCA<br>GATTTAA  | A | G | Ser | Ser | SILENT-<br>CODING | ATPase_<br>associat<br>ed | Human Gene Homologous to<br>SPTREMBL-ID:Q22494 SIMILAR<br>TOS. CEREBISIAE VACUOLAR H(+)-<br>ATPASE 54 KD SUBUNIT -<br>CAENORHABDITIS ELEGANS, 470<br>aa.  | 5.60E-108 | 8  |
| 330 | cg43967912 | 773  | ATTTGTGCACAG<br>GACTCCATTCCA<br>A[C]TJCTTCCAG<br>ATTTAAGTTCTG<br>AACTGT | C | T | Arg | Arg | SILENT-<br>CODING | ATPase_<br>associat<br>ed | Human Gene Homologous to<br>SPTREMBL-ID:Q22494 SIMILAR<br>TOS. CEREBISIAE VACUOLAR H(+)-<br>ATPASE 54 KD SUBUNIT -<br>CAENORHABDITIS ELEGANS, 470<br>aa.  | 5.60E-108 | 8  |
| 331 | cg43132502 | 371  | AGTGGGTGGCA<br>CCGCCGAGGCT<br>GCT[G/A]TTACG<br>GCTCATCTTCAT<br>TGATTTGC | G | A | Leu | Leu | SILENT-<br>CODING | ATPase_<br>associat<br>ed | Human Gene Similar to SPTREMBL-<br>ID:Q15332 GAMMA SUBUNIT OF<br>SODIUM POTASSIUM ATPASE LIKE<br>- HOMO SAPIENS (HUMAN), 126 aa.  | 9.40E-58  | 11 |

|     |            |      |   |   |   |     |     |                   |               |   |           |               |
|-----|------------|------|---|---|---|-----|-----|-------------------|---------------|---|-----------|---------------|
| 332 | cg44924856 | 352  | ACACGCCAGC<br>AGCCGAATGAT<br>GTTT[G]GGGTC<br>CTTGAGCCTCG<br>ACATGATCT   | T | G | Pro | Pro | SILENT-<br>CODING | cadherin      | Human Gene Similar to SWISSPROT-<br>ID:Q08345 EPITHELIAL DISCOIDIN<br>DOMAIN RECEPTOR 1<br>PRECURSOR (EC 2.7.1.112)<br>(TYROSINE-PROTEIN KINASE CAK)<br>(CELL ADHESION KINASE)<br>(TYROSINE KINASE DDR)<br>(DISCOIDIN RECEPTOR TYROSINE<br>KINASE) (TRK E) (PROTEIN-<br>TYROSINE KINASE RTK 6) - HOMO<br>SAPIENS (HUMAN), 913 aa. | 7.90E-77  | 6 (6q16)      |
| 333 | cg43991318 | 2634 | AGCACTCCCCT<br>GGCTCACCCCT<br>CTCT[C]CCTCG<br>TGGTCCCTTTTC<br>ACCTGGTG  | T | C | Ser | Ser | SILENT-<br>CODING | collagen      | Human Gene Similar to SWISSPROT-<br>ID:Q07092 COLLAGEN ALPHA<br>1(XVI) CHAIN PRECURSOR - HOMO<br>SAPIENS (HUMAN), 1603 aa.  | 1.30E-73  | 1 (1p34)      |
| 334 | cg41553795 | 480  | CTGTGCACGTG<br>GTTGTCGCTGA<br>GAC[C/T]GACTA<br>CCAGAGTTTCG<br>CTGTCCTGT | C | T | Thr | Thr | SILENT-<br>CODING | complement    | Human Gene Homologous to<br>SWISSPROT-ID:P07360<br>COMPLEMENT C8 GAMMA CHAIN<br>PRECURSOR - HOMO SAPIENS<br>(HUMAN), 202 aa.  | 1.40E-104 | 9<br>(9q34.3) |
| 335 | cg43973728 | 286  | GCAAAATTCAGAT<br>GCAAAGCCGTG<br>GC[C/T]AACGGG<br>AAGGTTCTCCG<br>AATGATC | C | T | Ala | Ala | SILENT-<br>CODING | cyclin        | Human Gene SWISSPROT-<br>ID:P51946 CYCLIN H (MO15-<br>ASSOCIATED PROTEIN) (P37) (P34)<br>- HOMO SAPIENS (HUMAN), 323 aa.  | 2.60E-172 | 5<br>(5q13.3) |
| 336 | cg43312829 | 1413 | TCCAATCAAAGA<br>CAACAGGACTC<br>CA[T/C]GTAAC<br>GAATATGAGGA<br>CAATTTGA  | T | C | His | His | SILENT-<br>CODING | dehydrogenase | Human Gene SWISSPROT-<br>ID:Q16134 ELECTRON TRANSFER<br>FLAVOPROTEIN-UBIQUINONE<br>OXIDOREDUCTASE PRECURSOR<br>(EC 1.5.5.1) (ETF-QO) (ETF-<br>UBIQUINONE OXIDOREDUCTASE)<br>(ETF DEHYDROGENASE)<br>(ELECTRON-TRANSFERRING-<br>FLAVOPROTEIN<br>DEHYDROGENASE) - HOMO<br>SAPIENS (HUMAN), 617 aa.                                   | 0.00E+00  | 4             |

|     |            |      |  |   |   |     |                   |                   |   |          |   |
|-----|------------|------|--|---|---|-----|-------------------|-------------------|---|----------|---|
| 337 | cg43312829 | 1422 | AGACAAACAGGA<br>CTCCATGTAAC<br>GATGATGAG<br>GACAAATTTGAAG<br>AAATCAT   | A | G | Glu | SILENT-<br>CODING | dehydrog<br>enase | Human Gene SWISSPROT-<br>ID:Q16134 ELECTRON TRANSFER<br>FLAVOPROTEIN-UBIQUINONE<br>OXIDOREDUCTASE PRECURSOR<br>(EC 1.5.5.1) (ETF-QO) (ETF-<br>UBIQUINONE OXIDOREDUCTASE)<br>(ETF DEHYDROGENASE)<br>(ELECTRON-TRANSFERRING-<br>FLAVOPROTEIN<br>DEHYDROGENASE) - HOMO<br>SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |
| 338 | cg43312829 | 1452 | AGGACAAATTTGA<br>AGAAATCATGG<br>GTATGTTGAAA<br>GAGCTATATTCT<br>GTTAGAA | A | G | Val | SILENT-<br>CODING | dehydrog<br>enase | Human Gene SWISSPROT-<br>ID:Q16134 ELECTRON TRANSFER<br>FLAVOPROTEIN-UBIQUINONE<br>OXIDOREDUCTASE PRECURSOR<br>(EC 1.5.5.1) (ETF-QO) (ETF-<br>UBIQUINONE OXIDOREDUCTASE)<br>(ETF DEHYDROGENASE)<br>(ELECTRON-TRANSFERRING-<br>FLAVOPROTEIN<br>DEHYDROGENASE) - HOMO<br>SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |
| 339 | cg43312829 | 1473 | GGGTATGGAAA<br>GAGCTATATTCT<br>GTTCJAGAAATA<br>TAAGGCCATCCT<br>GCCACG  | T | C | Val | SILENT-<br>CODING | dehydrog<br>enase | Human Gene SWISSPROT-<br>ID:Q16134 ELECTRON TRANSFER<br>FLAVOPROTEIN-UBIQUINONE<br>OXIDOREDUCTASE PRECURSOR<br>(EC 1.5.5.1) (ETF-QO) (ETF-<br>UBIQUINONE OXIDOREDUCTASE)<br>(ETF DEHYDROGENASE)<br>(ELECTRON-TRANSFERRING-<br>FLAVOPROTEIN<br>DEHYDROGENASE) - HOMO<br>SAPIENS (HUMAN). 617 aa. | 0.00E+00 | 4 |

|     |            |      |  |   |   |     |     |                   |                   |   |           |    |
|-----|------------|------|--|---|---|-----|-----|-------------------|-------------------|---|-----------|----|
| 340 | cg43312829 | 1569 | ACTGGATATTGA<br>GAGGAATGGAG<br>CC[G/A]TGGACT<br>CTAAACATAAA<br>GGCTCTG   | G | A | Pro | Pro | SILENT-<br>CODING | dehydrog<br>enase | Human Gene SWISSPROT-<br>ID:Q16134 ELECTRON TRANSFER<br>FLAVOPROTEIN-UBIQUINONE<br>OXIDOREDUCTASE PRECURSOR<br>(EC 1.5.5.1) (ETF-QO) (ETF-<br>UBIQUINONE OXIDOREDUCTASE)<br>(ETF DEHYDROGENASE)<br>(ELECTRON-TRANSFERRING-<br>FLAVOPROTEIN<br>DEHYDROGENASE) - HOMO<br>SAPIENS (HUMAN), 617 aa. | 0.00E+00  | 4  |
| 341 | cg43312829 | 1623 | TTGAACGGCTC<br>AAGCCAGCCAA<br>GGA[T/C]TGAC<br>ACCCATTGAGTA<br>TCCAAAC    | T | C | Asp | Asp | SILENT-<br>CODING | dehydrog<br>enase | Human Gene SWISSPROT-<br>ID:Q16134 ELECTRON TRANSFER<br>FLAVOPROTEIN-UBIQUINONE<br>OXIDOREDUCTASE PRECURSOR<br>(EC 1.5.5.1) (ETF-QO) (ETF-<br>UBIQUINONE OXIDOREDUCTASE)<br>(ETF DEHYDROGENASE)<br>(ELECTRON-TRANSFERRING-<br>FLAVOPROTEIN<br>DEHYDROGENASE) - HOMO<br>SAPIENS (HUMAN), 617 aa. | 0.00E+00  | 4  |
| 342 | cg43307992 | 652  | TCGAGGGCCCC<br>AACTTTGAGTTC<br>TC[C/A]ACGGAG<br>ACCCATGAGGA<br>GCTGCTGT  | C | A | Ser | Ser | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Homologous to<br>SPTREMBL-ID:O00217<br>MITOCHONDRIAL NADH<br>DEHYDROGENASE-UBIQUINONE<br>FE-S PROTEIN 8, 23 KDA SUBUNIT<br>PRECURSOR - HOMO SAPIENS<br>(HUMAN), 210 aa.  | 1.70E-113 | 11 |
| 343 | cg43969759 | 965  | TGGCTGTGGGC<br>TTCACCCAGCCTC<br>AC[C/T]ACCTCC<br>TCCAGGGAGTT<br>GACTTCAG | C | T | Val | Val | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Homologous to<br>SPTREMBL-ID:Q16797 NADP-<br>DEPENDENT MALIC ENZYME (EC<br>1.1.1.40) (MALATE<br>DEHYDROGENASE<br>(OXALOACETATE<br>DECARBOXYLATING) (NADP+))<br>(PYRUVIC-MALIC CARBOXYLASE) -<br>HOMO SAPIENS (HUMAN), 572 aa.  | 1.80E-109 | 11 |

|     |            |     |   |   |   |     |     |                   |                   |  |          |  |
|-----|------------|-----|---|---|---|-----|-----|-------------------|-------------------|--|----------|--|
| 344 | cg39523614 | 318 | ATGCTGGATCA<br>GATCCAGCTGC<br>ACTATTAAGTGT<br>CGAGCCGACGA<br>AGATGGGG   | A | T | Leu | Leu | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Similar to SWISSPROT-<br>ID:P46703 ACYL-COA<br>DEHYDROGENASE (EC 1.3.99.-) -<br>MYCOBACTERIUM LEPRAE, 389 aa.                                 | 2.10E-76 |  |
| 345 | cg39523614 | 360 | AAGATGGGGAC<br>AGTTTCGTCCTG<br>AA[C/T]GGCGTC<br>AAGGCTTGGGT<br>CACGGAGG | C | T | Asn | Asn | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Similar to SWISSPROT-<br>ID:P46703 ACYL-COA<br>DEHYDROGENASE (EC 1.3.99.-) -<br>MYCOBACTERIUM LEPRAE, 389 aa.                                 | 2.10E-76 |  |
| 346 | cg39523614 | 366 | GGGACAGTTTC<br>GTCCTGAACGG<br>CGT[C/T]AAGGC<br>TTGGGTCACGG<br>AGGCTGGCG | C | T | Val | Val | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Similar to SWISSPROT-<br>ID:P46703 ACYL-COA<br>DEHYDROGENASE (EC 1.3.99.-) -<br>MYCOBACTERIUM LEPRAE, 389 aa.                                 | 2.10E-76 |  |
| 347 | cg39523614 | 613 | TCAGGGGCACG<br>GTCTGAGTGTT<br>GCTT[C/T]GGGT<br>ACGCTTGACAA<br>CTCTCGTGT | T | C | Leu | Leu | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Similar to SWISSPROT-<br>ID:P46703 ACYL-COA<br>DEHYDROGENASE (EC 1.3.99.-) -<br>MYCOBACTERIUM LEPRAE, 389 aa.                                 | 2.10E-76 |  |
| 348 | cg39523614 | 660 | GTGTCGATTGG<br>CTGCTCAAGCA<br>GT[G/A]GGAATT<br>GCCCAGGGAGC<br>TTTAGACA  | G | A | Val | Val | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Similar to SWISSPROT-<br>ID:P46703 ACYL-COA<br>DEHYDROGENASE (EC 1.3.99.-) -<br>MYCOBACTERIUM LEPRAE, 389 aa.                                 | 2.10E-76 |  |
| 349 | cg42717491 | 207 | AGGCTCACACT<br>CACTTCATGTTT<br>TT[C/G]ACAAAG<br>TCCTCGCCTTTC<br>TTGATGG | C | G | Val | Val | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Similar to SWISSPROT-<br>ID:P04636 MALATE<br>DEHYDROGENASE,<br>MITOCHONDRIAL PRECURSOR (EC<br>1.1.1.37) - RATTUS NORVEGICUS<br>(RAT), 338 aa. | 2.40E-52 |  |



|     |            |      |  |   |   |     |     |                   |                   |  |           |    |
|-----|------------|------|--|---|---|-----|-----|-------------------|-------------------|--|-----------|----|
| 350 | cg42717491 | 252  | TGATGGAGGCT<br>TTCAGCTCAGG<br>GAT[G/A]GCCTC<br>GGCAATCATTTT<br>CTCCTCAA  | G | A | Ala | Ala | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Similar to SWISSPROT-<br>ID:P04636 MALATE<br>DEHYDROGENASE,<br>MITOCHONDRIAL PRECURSOR (EC<br>1.1.1.37) - RATTUS NORVEGICUS<br>(RAT), 338 aa.   | 2.40E-52  |    |
| 351 | cg42717491 | 270  | CAGGGATGGCC<br>TCGGCAATCATT<br>TT[C/T]TCCTCAA<br>AAGGAGTGATTT<br>TGCCAA  | C | T | Glu | Glu | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Similar to SWISSPROT-<br>ID:P04636 MALATE<br>DEHYDROGENASE,<br>MITOCHONDRIAL PRECURSOR (EC<br>1.1.1.37) - RATTUS NORVEGICUS<br>(RAT), 338 aa.   | 2.40E-52  |    |
| 352 | cg42717491 | 288  | TCATTTTCTCCT<br>CAAAAGGAGTG<br>ATT[C/T]TGCCAA<br>TGCCTAGGTTCT<br>TCTCCA  | T | C | Lys | Lys | SILENT-<br>CODING | dehydrog<br>enase | Human Gene Similar to SWISSPROT-<br>ID:P04636 MALATE<br>DEHYDROGENASE,<br>MITOCHONDRIAL PRECURSOR (EC<br>1.1.1.37) - RATTUS NORVEGICUS<br>(RAT), 338 aa.   | 2.40E-52  |    |
| 353 | cg42711596 | 1535 | ATTAGTATGCT<br>GTGAGCTGCTT<br>TT[G]GTTGAATC<br>TGATTAGTTTC<br>AGTTTC     | T | G | Thr | Thr | SILENT-<br>CODING | eph               | Human Gene Homologous to<br>SWISSPROT-ID:P48722 OSMOTIC<br>STRESS PROTEIN 94 (HEAT<br>SHOCK 70-RELATED PROTEIN APG-<br>1) - MUS MUSCULUS (MOUSE), 838<br>aa.   | 2.10E-115 | 4  |
| 354 | cg43319420 | 1557 | AGAAAGTCAGAA<br>GGCCTTCCTGT<br>GGC[A/C]CCGTT<br>CATGGACCGAG<br>ACAAAGTGA | A | C | Ala | Ala | SILENT-<br>CODING | esterase          | Human Gene Similar to SWISSNEW-<br>ID:Q23917 3':5'-CYCLIC-<br>NUCLEOTIDE<br>PHOSPHODIESTERASE REGA (EC<br>3.1.4.17) (PDEASE REGA) -<br>DICTYOSTELIUM DISCOIDEUM<br>(SLIME MOLD), 793<br>aa.   pcis:SWISSPROT-ID:Q23917 3':5'-<br>CYCLIC-NUCLEOTIDE<br>PHOSPHODIESTERASE REGA (EC<br>3.1.4.17) (PDEASE REGA) -<br>DICTYOSTELIUM DISCOIDEUM<br>(SLIME MOLD), 793 aa. | 3.30E-60  | 21 |

|     |            |      |   |   |   |     |     |                   |              |  |           |    |
|-----|------------|------|---|---|---|-----|-----|-------------------|--------------|--|-----------|----|
| 355 | cg41029366 | 687  | AGTGGGGATCA<br>GTGTGCGATGA<br>CAC[T/C]TGGA<br>CCTGGAGGACG<br>CCCACGTGG  | T | C | Thr | Thr | SILENT-<br>CODING | glycoprotein | Human Gene SPTREMBL-ID:Q61003<br>T CELL SURFACE GLYCOPROTEIN<br>CD6 - MUS MUSCULUS (MOUSE),<br>665 aa.   | 1.00E-234 | 11 |
| 356 | cg42876034 | 860  | GCGCCCGCCGC<br>GGCAGCGCCCC<br>GAG[G/C]CCGGC<br>TTCGGCCCGCA<br>GCCTGGACG | G | C | Gly | Gly | SILENT-<br>CODING | glycoprotein | Human Gene Similar to SWISSPROT-<br>ID:Q07066 22 KD PEROXISOMAL<br>MEMBRANE PROTEIN - RATTUS<br>NORVEGICUS (RAT), 193 aa.  | 2.60E-78  |    |
| 357 | cg43976227 | 258  | CTGGTGTGATCT<br>CTGTCTCTTTAT<br>G[G/A]ACCACTA<br>CTTTGGTCACTG<br>ACATGT | G | A | Val | Val | SILENT-<br>CODING | glycoprotein | Human Gene Similar to SPTREMBL-<br>ID:Q14245 ERYTHROID<br>MEMBRANE PROTEIN 4.1 - HOMO<br>SAPIENS (HUMAN), 641 aa.  | 2.60E-60  | 18 |
| 358 | cg43916642 | 816  | GGCTGAAAAGC<br>ATATCTATACAT<br>TC[G/A]GAGAAG<br>TCGCAATAGAA<br>AGGAAA   | G | A | Ser | Ser | SILENT-<br>CODING | helicase     | Human Gene Similar to SWISSPROT-<br>ID:P25888 PUTATIVE ATP-<br>DEPENDENT RNA HELICASE RHLE-<br>ESCHERICHIA COLI, 454 aa.   | 2.90E-54  | 1  |
| 359 | cg43925670 | 2320 | AACCAGCATCA<br>CCTCGGAACCTT<br>TC[T/C]TCCATCA<br>AGTCAGCAATCT<br>GAATTT | T | C | Glu | Glu | SILENT-<br>CODING | interferon   | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa. lpcds:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0.00E+00  | 1  |

|     |            |      |  |   |   |     |     |                   |            |   |          |   |
|-----|------------|------|--|---|---|-----|-----|-------------------|------------|---|----------|---|
| 360 | cg43925670 | 2370 | TTGTCATACCTCT<br>TCTCTCATTTT<br>AAGGATTAAGTT<br>TTAAATCGTTGC<br>TCAGT  | A | G | Leu | Leu | SILENT-<br>CODING | interferon | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.lpcIs:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0.00E+00 | 1 |
| 361 | cg43925670 | 2389 | TTTTTAAATTAA<br>GTTTAAATCGT<br>T[G/A]CTCAGTA<br>AGGACTTAACCA<br>TTCTAA | G | A | Ser | Ser | SILENT-<br>CODING | interferon | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.lpcIs:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0.00E+00 | 1 |
| 362 | cg43925670 | 2446 | AATCATTGATGA<br>CCTCTAATCCTT<br>TTT/CJAGTAGAA<br>CAATGTTCTTGT<br>ATTTT | T | C | Leu | Leu | SILENT-<br>CODING | interferon | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.lpcIs:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0.00E+00 | 1 |

|     |            |      |   |   |   |     |     |                   |           |  |           |               |
|-----|------------|------|---|---|---|-----|-----|-------------------|-----------|--|-----------|---------------|
| 363 | cg44004587 | 1913 | TTTATTGTCAT<br>TTTCATCAATAA<br>G[G/A]ATACACA<br>TCTCTGCCAGG<br>AGTIGAA  | G | A | Ile | Ile | SILENT-<br>CODING | isomerase | Human Gene Homologous to<br>SPTREMBL-ID:Q13907 HOMOLOG<br>OF YEAST IPP ISOMERASE - HOMO<br>SAPIENS (HUMAN), 228 aa.  | 3.00E-123 |               |
| 364 | cg43257400 | 2144 | CATGTGTGGTAA<br>CTCCTCAAGATG<br>G[G/C]GAGACGT<br>TAGCACAAATGA<br>TAGAAG | G | C | Gly | Gly | SILENT-<br>CODING | kinase    | Human Gene SPTREMBL-ID:Q60680<br>CONSERVED HELIX-LOOP-HELIX<br>UBIQUITOUS KINASE - MUS<br>MUSCULUS (MOUSE), 745 aa.  | 0.00E+00  | 10            |
| 365 | cg43931272 | 2072 | TTGGTGGTCTT<br>TCCCAACCACAA<br>A[A/G]CACTCCG<br>GTGGTAAATACC<br>AATAAG  | A | G | Cys | Cys | SILENT-<br>CODING | kinase    | Human Gene TREMBLNEW-<br>ID:G2853031 TOUSLED-LIKE<br>KINASE - MUS MUSCULUS<br>(MOUSE), 717 aa.   | 0.00E+00  |               |
| 366 | cg42665067 | 748  | GGGCTTCTAC<br>ATATCCCCCCG<br>AAG[C/T]ACCTT<br>CAGCACTCTGC<br>AGGAGCTGG  | C | T | Ser | Ser | SILENT-<br>CODING | kinase    | Human Gene SWISSPROT-<br>ID:P08631 TYROSINE-PROTEIN<br>KINASE HCK (EC 2.7.1.12) (P59-<br>HCK AND P60-HCK) (HEMOPOIETIC<br>CELL KINASE) - HOMO SAPIENS<br>(HUMAN), 526 aa.  | 9.20E-289 | 20<br>(20q11) |
| 367 | cg43982923 | 634  | CGATGCAGAAA<br>TACGAGAAACT<br>GGA[A/G]AAGAT<br>TGGGGAAGGCA<br>CCTACGGAA | A | G | Glu | Glu | SILENT-<br>CODING | kinase    | Human Gene SWISSPROT-<br>ID:P49615 CELL DIVISION PROTEIN<br>KINASE 5 (EC 2.7.1.-) (TAU<br>PROTEIN KINASE II CATALYTIC<br>SUBUNIT) (TPKII CATALYTIC<br>SUBUNIT) (KINASE PSSALRE)<br>(CRK6) - MUS MUSCULUS<br>(MOUSE), 292 aa. | 3.60E-159 | 19            |
| 368 | cg43982923 | 655  | TGGAAGGATTG<br>GGGAAGGCACC<br>TA[C/T]GGAAC<br>GTGTTCAAGGC<br>CAAAAACC   | C | T | Tyr | Tyr | SILENT-<br>CODING | kinase    | Human Gene SWISSPROT-<br>ID:P49615 CELL DIVISION PROTEIN<br>KINASE 5 (EC 2.7.1.-) (TAU<br>PROTEIN KINASE II CATALYTIC<br>SUBUNIT) (TPKII CATALYTIC<br>SUBUNIT) (KINASE PSSALRE)<br>(CRK6) - MUS MUSCULUS<br>(MOUSE), 292 aa. | 3.60E-159 | 19            |

|     |            |     |  |   |   |     |     |                   |                     |  |           |    |
|-----|------------|-----|--|---|---|-----|-----|-------------------|---------------------|--|-----------|----|
| 369 | cg43982923 | 697 | CCAAAACCGG<br>GAGACTCATGA<br>GATC/TGTGGC<br>TCTGAAACGGG<br>TGAGGCTGG     | C | T | Ile | Ile | SILENT-<br>CODING | kinase              | Human Gene SWISSPROT-<br>ID:P49615 CELL DIVISION PROTEIN<br>KINASE 5 (EC 2.7.1.-) (TAU<br>PROTEIN KINASE II CATALYTIC<br>SUBUNIT) (TPKII CATALYTIC<br>SUBUNIT) (KINASE PSSALRE)<br>(CRK6) - MUS MUSCULUS<br>(MOUSE), 292 aa. | 3.60E-159 | 19 |
| 370 | cg43919086 | 576 | CGCTCAGGAGG<br>ATATAGGTGATG<br>AC/A/GCCGATG<br>CTCCACATGTCC<br>GCCTCCA   | A | G | Gly | Gly | SILENT-<br>CODING | kinase              | Human Gene TREMBLNEW-<br>ID:D1025880 ZIP-KINASE - HOMO<br>SAPIENS (HUMAN), 454 aa.   | 6.80E-158 | 19 |
| 371 | cg25143358 | 407 | GGCGGCTTCA<br>AGTTTCGTGGTC<br>AT[G/A]CCGCCG<br>GTTCCACACCC<br>CGAACCCAG  | G | A | Gly | Gly | SILENT-<br>CODING | kinase              | Human Gene Similar to SWISSPROT-<br>ID:P46546 GLUTAMATE 5-KINASE<br>(EC 2.7.2.11) (GAMMA-GLUTAMYL<br>KINASE) (GK) -<br>CORYNEBACTERIUM<br>GLUTAMICUM, 369 aa.  | 2.70E-51  |    |
| 372 | cg43105476 | 514 | GGTCCGATGC<br>CCCACATTGCT<br>GGC[C/T]GTGTG<br>CTTCACCAGGA<br>ACTCCACCA   | C | T | Thr | Thr | SILENT-<br>CODING | kinasein<br>hibitor | Human Gene Similar to SWISSPROT-<br>ID:P42773 CYCLIN-DEPENDENT<br>KINASE 6 INHIBITOR (P18-INK6) -<br>HOMO SAPIENS (HUMAN), 168 aa.   | 7.80E-86  |    |
| 373 | cg43105476 | 541 | TGTGCTTCACCA<br>GGAACCTCCACC<br>AC[C/A]CGGAGG<br>TGGCCTTCTTTG<br>GCAGCCA | C | A | Arg | Arg | SILENT-<br>CODING | kinasein<br>hibitor | Human Gene Similar to SWISSPROT-<br>ID:P42773 CYCLIN-DEPENDENT<br>KINASE 6 INHIBITOR (P18-INK6) -<br>HOMO SAPIENS (HUMAN), 168 aa.   | 7.80E-86  |    |
| 374 | cg43105476 | 595 | GCAAGGCGCAGG<br>TTCCCTTCATTA<br>TC[C/T]TCGATGT<br>TAACATCAGCTT<br>GAAACT | C | T | Glu | Glu | SILENT-<br>CODING | kinasein<br>hibitor | Human Gene Similar to SWISSPROT-<br>ID:P42773 CYCLIN-DEPENDENT<br>KINASE 6 INHIBITOR (P18-INK6) -<br>HOMO SAPIENS (HUMAN), 168 aa.   | 7.80E-86  |    |

|     |            |     |   |   |   |     |     |                   |                     |   |          |               |
|-----|------------|-----|---|---|---|-----|-----|-------------------|---------------------|---|----------|---------------|
| 375 | cg43105476 | 616 | TATCCTCGATGT<br>TAACATCAGCTT<br>GTA/GAACTCCA<br>GCAAAGTCTGTA<br>AAGTGT  | A | G | Phe | Phe | SILENT-<br>CODING | kinasere<br>hibitor | Human Gene Similar to SWISSPROT-<br>ID:P42773 CYCLIN-DEPENDENT<br>KINASE 6 INHIBITOR (P18-INK6) -<br>HOMO SAPIENS (HUMAN), 168 aa.  | 7.80E-86 |               |
| 376 | cg43939695 | 410 | CAGGGAACAGC<br>AATGGGAACGC<br>CAGT/CJATCAA<br>CATCACGGACA<br>TCTCAAGGA  | T | C | Ser | Ser | SILENT-<br>CODING | kinasere<br>ceptor  | Human Gene SWISSPROT-<br>ID:Q16288 NT-3 GROWTH FACTOR<br>RECEPTOR PRECURSOR (EC<br>2.7.1.112) (TRKC TYROSINE<br>KINASE) (GP145-TRKC) (TRK-C) -<br>HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15<br>(15q25) |
| 377 | cg43939695 | 419 | GCAATGGGAAC<br>GCCAGTATCAA<br>CATC/TJACGGA<br>CATCTCAAGGAA<br>TATCACTT  | C | T | Ile | Ile | SILENT-<br>CODING | kinasere<br>ceptor  | Human Gene SWISSPROT-<br>ID:Q16288 NT-3 GROWTH FACTOR<br>RECEPTOR PRECURSOR (EC<br>2.7.1.112) (TRKC TYROSINE<br>KINASE) (GP145-TRKC) (TRK-C) -<br>HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15<br>(15q25) |
| 378 | cg43939695 | 467 | CTTCCATACACA<br>TAGAGAACTGG<br>CGC/AJAGTCTT<br>CACACGCTCAA<br>CGCCGTGG  | C | A | Arg | Arg | SILENT-<br>CODING | kinasere<br>ceptor  | Human Gene SWISSPROT-<br>ID:Q16288 NT-3 GROWTH FACTOR<br>RECEPTOR PRECURSOR (EC<br>2.7.1.112) (TRKC TYROSINE<br>KINASE) (GP145-TRKC) (TRK-C) -<br>HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15<br>(15q25) |
| 379 | cg43939695 | 473 | TACACATAGAGA<br>ACTGGCGCAGT<br>CTT/GJCACACG<br>CTCAACGCCGT<br>GGACATGG  | T | G | Leu | Leu | SILENT-<br>CODING | kinasere<br>ceptor  | Human Gene SWISSPROT-<br>ID:Q16288 NT-3 GROWTH FACTOR<br>RECEPTOR PRECURSOR (EC<br>2.7.1.112) (TRKC TYROSINE<br>KINASE) (GP145-TRKC) (TRK-C) -<br>HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15<br>(15q25) |
| 380 | cg43939695 | 479 | TAGAGAACTGG<br>CGCAGTCTTCA<br>CAC[G/A]CTCAA<br>CGCCGTGGACA<br>TGGAGCTCT | G | A | Thr | Thr | SILENT-<br>CODING | kinasere<br>ceptor  | Human Gene SWISSPROT-<br>ID:Q16288 NT-3 GROWTH FACTOR<br>RECEPTOR PRECURSOR (EC<br>2.7.1.112) (TRKC TYROSINE<br>KINASE) (GP145-TRKC) (TRK-C) -<br>HOMO SAPIENS (HUMAN), 839 aa. | 0.00E+00 | 15<br>(15q25) |







|     |            |      |   |   |   |     |     |                   |          |   |           |   |
|-----|------------|------|---|---|---|-----|-----|-------------------|----------|---|-----------|---|
| 394 | cg44929972 | 1266 | ATGTCCTGAGG<br>GCAGTGGAGGA<br>ACG[A]GATTT<br>TCCAACAGAAAC<br>CATTAAAT   | G | A | Arg | Arg | SILENT-<br>CODING | ngf      | Human Gene TREMBLNEW-<br>ID:E1216872 NERVE GROWTH<br>FACTOR-INDUCIBLE PC4<br>HOMOLOGUE - HOMO SAPIENS<br>(HUMAN), 453 aa.   | 4.70E-214 | 7 |
| 395 | cg44926604 | 1283 | AGTCGATGTCC<br>AGCTTGCGGGC<br>CACG[A]CGGTG<br>TAGATTGGGCA<br>GGTTCAGCT  | G | A | Arg | Arg | SILENT-<br>CODING | nuclease | Human Gene SWISSPROT-<br>ID:Q01831 DNA-REPAIR PROTEIN<br>COMPLEMENTING XP-C CELLS<br>(XERODERMA PIGMENTOSUM<br>GROUP C COMPLEMENTING<br>PROTEIN) (P125) - HOMO SAPIENS<br>(HUMAN), 939 aa.  | 0.00E+00  | 3 |
| 396 | cg38642684 | 282  | GCCAGTTAATAT<br>TGCCTAGTAATT<br>TTC/TJTGATAATC<br>ATTTAAGGTATG<br>TAAGT | C | T | Gln | Gln | SILENT-<br>CODING | nuclease | Human Gene Similar to SWISSNEW-<br>ID:P10266 RETROVIRUS-RELATED<br>POL POLYPROTEIN [CONTAINS:<br>REVERSE TRANSCRIPTASE (EC<br>2.7.7.49); ENDONUCLEASE] -<br>HOMO SAPIENS (HUMAN), 874<br>aa.[pcis:SWISSPROT-ID:P10266<br>RETROVIRUS-RELATED POL<br>POLYPROTEIN (REVERSE<br>TRANSCRIPTASE (EC 2.7.7.49);<br>ENDONUCLEASE) - HOMO<br>SAPIENS (HUMAN), 874 aa. | 2.60E-50  |   |
| 397 | cg38642684 | 387  | AAGGATACTTCC<br>AAGGAGAGGAC<br>ATT/CJTGACTT<br>TTTCAGGTGCAA<br>TGATTA   | T | C | Gln | Gln | SILENT-<br>CODING | nuclease | Human Gene Similar to SWISSNEW-<br>ID:P10266 RETROVIRUS-RELATED<br>POL POLYPROTEIN [CONTAINS:<br>REVERSE TRANSCRIPTASE (EC<br>2.7.7.49); ENDONUCLEASE] -<br>HOMO SAPIENS (HUMAN), 874<br>aa.[pcis:SWISSPROT-ID:P10266<br>RETROVIRUS-RELATED POL<br>POLYPROTEIN (REVERSE<br>TRANSCRIPTASE (EC 2.7.7.49);<br>ENDONUCLEASE) - HOMO<br>SAPIENS (HUMAN), 874 aa. | 2.60E-50  |   |

|     |            |      |  |   |   |     |     |                   |          |   |          |          |
|-----|------------|------|--|---|---|-----|-----|-------------------|----------|---|----------|----------|
| 398 | cg38642684 | 405  | AGGACATTTGTA<br>CTTTTCAGGTG<br>C/A/TJATGATTAA<br>ACCACTTAACTG<br>TGCAT   | A | T | Ile | Ile | SILENT-<br>CODING | nuclease | Human Gene Similar to SWISSNEW-<br>ID:P10266 RETROVIRUS-RELATED<br>POL POLYPROTEIN [CONTAINS:<br>REVERSE TRANSCRIPTASE (EC<br>2.7.7.49); ENDONUCLEASE] -<br>HOMO SAPIENS (HUMAN), 874<br>aa. pcis:SWISSPROT-ID:P10266<br>RETROVIRUS-RELATED POL<br>POLYPROTEIN (REVERSE<br>TRANSCRIPTASE (EC 2.7.7.49);<br>ENDONUCLEASE) - HOMO<br>SAPIENS (HUMAN), 874 aa. | 2.60E-50 |          |
| 399 | cg38642684 | 456  | TCCTTATGACAG<br>AGGTATATAAAC<br>TTT/CJAAAAAGCA<br>CTGGCTCCACT<br>GGGGCTG | T | C | Leu | Leu | SILENT-<br>CODING | nuclease | Human Gene Similar to SWISSNEW-<br>ID:P10266 RETROVIRUS-RELATED<br>POL POLYPROTEIN [CONTAINS:<br>REVERSE TRANSCRIPTASE (EC<br>2.7.7.49); ENDONUCLEASE] -<br>HOMO SAPIENS (HUMAN), 874<br>aa. pcis:SWISSPROT-ID:P10266<br>RETROVIRUS-RELATED POL<br>POLYPROTEIN (REVERSE<br>TRANSCRIPTASE (EC 2.7.7.49);<br>ENDONUCLEASE) - HOMO<br>SAPIENS (HUMAN), 874 aa. | 2.60E-50 |          |
| 400 | cg43919677 | 2577 | TTGAAGTAGCTC<br>CTGAAGCTTCTA<br>C/G/AJTCTAGTG<br>CCAGCCCAAGTG<br>ATTGCTC | G | A | Thr | Thr | SILENT-<br>CODING | oncogene | Human Gene SWISSPROT-<br>ID:Q00918 LATENT<br>TRANSFORMING GROWTH<br>FACTOR BETA BINDING PROTEIN 1<br>PRECURSOR (TRANSFORMING<br>GROWTH FACTOR BETA-1<br>BINDING PROTEIN 1) (TGF-BETA1-<br>BP- 1) (TRANSFORMING GROWTH<br>FACTOR BETA-1 MASKING<br>PROTEIN, LARGE SUBUNIT) -<br>RATTUS NORVEGICUS (RAT), 1712<br>aa.   | 0.00E+00 | 2 (2p12) |

|     |            |      |  |   |   |     |                   |                 |   |           |               |
|-----|------------|------|--|---|---|-----|-------------------|-----------------|---|-----------|---------------|
| 401 | cg44005163 | 1384 | CCTGTGGGCTG<br>ATTACATTAACT<br>GAT/CJGCACAA<br>AGATTATGTAAT<br>GCTTTAT     | T | C | Asp | SILENT-<br>CODING | oncogen<br>e    | Human Gene SWISSPROT-<br>ID:P12756 SKI-RELATED<br>ONCOGENE SNOA - HOMO<br>SAPIENS (HUMAN), 415 aa.  | 5.30E-229 |               |
| 402 | cg44005163 | 1423 | GTAATGCTTTAT<br>TGCGGCCACGA<br>ACT/GJTTCCTC<br>AAATGGTAGC<br>GTACTTC       | T | G | Thr | SILENT-<br>CODING | oncogen<br>e    | Human Gene SWISSPROT-<br>ID:P12756 SKI-RELATED<br>ONCOGENE SNOA - HOMO<br>SAPIENS (HUMAN), 415 aa.  | 5.30E-229 |               |
| 403 | cg25334466 | 546  | TCAAGGACCCAG<br>TTCACCTACCCCTC<br>CC/T/CJGAGGTG<br>AAGGACTGATG<br>CTTTGCCA | T | C | Pro | SILENT-<br>CODING | oxidase         | Human Gene Homologous to<br>SWISSPROT-ID:P25689 URICASE<br>(EC 1.7.3.3) (URATE OXIDASE) -<br>PAPIO HAMADRYAS (HAMADRYAS<br>BABOON), 303 aa.   | 1.30E-149 |               |
| 404 | cg42535091 | 750  | AACTGAAATACGA<br>ACGTTGGTGGA<br>GG[A/G]GAACGG<br>TTTGATTCTTTG<br>ACAGATC   | A | G | Gly | SILENT-<br>CODING | phosphat<br>ase | Human Gene SWISSPROT-<br>ID:Q06124 PROTEIN-TYROSINE<br>PHOSPHATASE 2C (EC 3.1.3.48)<br>(PTP-2C) (PTP-1D) (SH-PTP3) (SH-<br>PTP2) - HOMO SAPIENS (HUMAN),<br>593 aa.   | 0.00E+00  | 12            |
| 405 | cg43302847 | 1227 | GGTGGTGGTGG<br>CCATCCAGATC<br>CTG[C/A]GGAAG<br>AACCCCAAAGG<br>CTTCTCTT     | C | A | Arg | SILENT-<br>CODING | phosphat<br>ase | Human Gene SWISSPROT-<br>ID:P05186 ALKALINE<br>PHOSPHATASE, TISSUE-<br>NONSPECIFIC ISOZYME<br>PRECURSOR (EC 3.1.3.1) (AP-<br>TNAP) (LIVER/BONE/KIDNEY<br>ISOZYME) (TNSALP) - HOMO<br>SAPIENS (HUMAN), 524 aa. | 3.20E-286 | 1<br>(1p36.1) |
| 406 | cg39728924 | 433  | GGCAAAATGGTG<br>TTGGAAAATAAT<br>TC[G/A]AATGTTA<br>TTGCCATGATAA<br>CCAGAG   | G | A | Ser | SILENT-<br>CODING | phosphat<br>ase | Human Gene Similar to<br>TREMBLINW-ID:D1024666<br>PROTEIN-TYROSINE-<br>PHOSPHATASE (EC 3.1.3.48) - MUS<br>MUSCULUS (MOUSE), 426 aa.   | 1.20E-64  |               |

|     |            |      |   |   |   |     |     |                   |                  |   |           |               |
|-----|------------|------|---|---|---|-----|-----|-------------------|------------------|---|-----------|---------------|
| 407 | cg42881873 | 1564 | ACCTGAAAGCG<br>AGCGACTGGAA<br>AGT[A/G]AACGG<br>CGCGGGTCATA<br>AAGTTAGCC   | A | G | Val | Val | SILENT-<br>CODING | protease         | Human Gene SWISSNEW-ID:P29122<br>SUBTILISIN-LIKE PROTEASE<br>PACE4 PRECURSOR (EC 3.4.21.-) -<br>HOMO SAPIENS (HUMAN), 969<br>aa. pcls:SWISSPROT-ID:P29122<br>SUBTILISIN-LIKE PROTEASE<br>PACE4 PRECURSOR (EC 3.4.21.-) -<br>HOMO SAPIENS (HUMAN), 969 aa.     | 0.00E+00  | 15<br>(15q26) |
| 408 | cg42913398 | 589  | CTGTTCCGTGG<br>ATGAGAAGATA<br>GTC[T/C]ACATTT<br>CTGAAATATTCT<br>GCTCTTG   | T | C | Val | Val | SILENT-<br>CODING | protease         | Human Gene SPTREMBL-ID:O00199<br>INTEGRAL MEMBRANE SERINE<br>PROTEASE SEPRASE - HOMO<br>SAPIENS (HUMAN), 760 aa.  | 0.00E+00  | 2             |
| 409 | cg44028327 | 793  | TTCGAATTACCT<br>ACTCAATTGTGC<br>A[A/G]ACGAATT<br>GTTCCAAAGAG<br>AATTTTC   | A | G | Gln | Gln | SILENT-<br>CODING | protease<br>nhib | Human Gene SWISSPROT-<br>ID:P01042 KININOGEN, HMW<br>PRECURSOR (ALPHA-2-THIOL<br>PROTEINASE INHIBITOR)<br>(CONTAINS: BRADYKININ) - HOMO<br>SAPIENS (HUMAN), 644 aa.   | 0.00E+00  | 3 (3q27)      |
| 410 | cg43979831 | 899  | CCTCAAGGACC<br>ACTCCCAAGA<br>CTT[C/T]TATGTT<br>GATGAGAACAC<br>AACAGTCC    | C | T | Phe | Phe | SILENT-<br>CODING | protease<br>nhib | Human Gene SWISSPROT-<br>ID:P29622 KALLISTATIN<br>PRECURSOR (KALLIKREIN<br>INHIBITOR) (PROTEASE INHIBITOR<br>4) - HOMO SAPIENS (HUMAN), 427<br>aa.  | 1.10E-228 | 14            |
| 411 | cg43987538 | 905  | ATCATCATAAGA<br>GAAGAATCATTT<br>TTT[A/J]CCAGTAG<br>CCCCACTACCAT<br>GAATGA | T | A | Gly | Gly | SILENT-<br>CODING | reductase        | Human Gene SWISSPROT-<br>ID:Q08257 QUINONE<br>OXIDOREDUCTASE (EC 1.6.5.5)<br>(NADPH:QUINONE REDUCTASE)<br>(ZETA- CRYSTALLIN) - HOMO<br>SAPIENS (HUMAN), 329 aa.   | 1.10E-171 | 1 (1p31)      |
| 412 | cg42717608 | 142  | CCACAAAGGTC<br>TATGTCCAGCAC<br>CT[G/T]CTGAAG<br>AGAGACAAAGA<br>ACACCTGT   | G | T | Leu | Leu | SILENT-<br>CODING | reductase        | Human Gene Similar to SWISSNEW-<br>ID:P37040 NADPH-CYTOCHROME<br>P450 REDUCTASE (EC 1.6.2.4)<br>(CPR) - MUS MUSCULUS (MOUSE),<br>677 aa. pcls:SWISSPROT-ID:P37040<br>NADPH-CYTOCHROME P450<br>REDUCTASE (EC 1.6.2.4) (CPR) -<br>MUS MUSCULUS (MOUSE), 677 aa. | 1.80E-51  |               |

|     |            |      |  |   |   |     |     |                   |        |   |           |                 |
|-----|------------|------|--|---|---|-----|-----|-------------------|--------|---|-----------|-----------------|
| 413 | cg43927378 | 4726 | ATCTGATGGAG<br>AACTACCAGATC<br>GTT/CJGTCAGC<br>AACCTGGCCAC<br>TGAGCGTG   | T | C | Val | Val | SILENT-<br>CODING | struct | Human Gene SPTREMBL-ID:Q13459<br>MYOSIN-IXB - HOMO SAPIENS<br>(HUMAN), 2022 aa.   | 0         | 2               |
| 414 | cg43945592 | 1503 | GGGCTCGGGCA<br>GGGTACACAAA<br>CTC/T/CJGTGGC<br>TGCAAAATCCCC<br>AGAGGAGC  | T | C | Thr | Thr | SILENT-<br>CODING | struct | Human Gene TREMBLNEW-<br>ID:G2961252 SUPERVILLIN - HOMO<br>SAPIENS (HUMAN), 1788 aa.  | 0         | 10              |
| 415 | cg43957486 | 1475 | CTGGGGCTCCC<br>CGCTGCCAGTG<br>CCC/A/GJGCCGG<br>CGCCGCCCTGC<br>AGGCAGACG  | A | G | Pro | Pro | SILENT-<br>CODING | struct | Human Gene SWISSPROT-<br>ID:P07204 THROMBOMODULIN<br>PRECURSOR (FETOMODULIN) (TM)<br>(CD141 ANTIGEN) - HOMO<br>SAPIENS (HUMAN), 575 aa.                   | 0.00E+00  | 20<br>(20p11.2) |
| 416 | cg44932934 | 815  | TGCTCGAGGAT<br>GTCAACCGCAT<br>GTC/G/AJCCCTGG<br>GGCGCTGGCCA<br>TTATCTTCG | G | A | Ser | Ser | SILENT-<br>CODING | struct | Human Gene SPTREMBL-ID:Q63358<br>MYOSIN HEAVY CHAIN - RATTUS<br>NORVEGICUS (RAT), 1980 aa.  | 2.10E-179 |                 |
| 417 | cg43100187 | 320  | AACGCCCTAGAG<br>GGGAGCTGGT<br>GGC/C/AJCATGA<br>GCCTGCCATCC<br>AGAATGTGC  | C | A | Ala | Ala | SILENT-<br>CODING | struct | Human Gene SWISSPROT-<br>ID:P02549 SPECTRIN ALPHA<br>CHAIN, ERYTHROCYTE - HOMO<br>SAPIENS (HUMAN), 2418 aa.   | 1.80E-169 |                 |
| 418 | cg42930605 | 333  | GGTCCATGCAC<br>ACCTTGTCCTTC<br>GA/G/AJCCCAGC<br>AGGGCCTTGAG<br>CATGGCAT  | G | A | Gly | Gly | SILENT-<br>CODING | struct | Human Gene Similar to SWISSPROT-<br>ID:P48788 TROPONIN I, FAST<br>SKELETAL MUSCLE (TROPONIN I,<br>FAST-TWITCH ISOFORM) - HOMO<br>SAPIENS (HUMAN), 181 aa. | 1E-92     | 11<br>(11p15.5) |
| 419 | cg42930605 | 411  | GGGGCCGCTTG<br>AACTTGCCCCCG<br>CAG/A/GJTCAAA<br>TAGCTTCTGGTT<br>CATGTCCT | A | G | Asp | Asp | SILENT-<br>CODING | struct | Human Gene Similar to SWISSPROT-<br>ID:P48788 TROPONIN I, FAST<br>SKELETAL MUSCLE (TROPONIN I,<br>FAST-TWITCH ISOFORM) - HOMO<br>SAPIENS (HUMAN), 181 aa. | 1E-92     | 11<br>(11p15.5) |



|     |            |     |   |   |   |     |     |                   |        |   |         |                 |
|-----|------------|-----|---|---|---|-----|-----|-------------------|--------|---|---------|-----------------|
| 427 | cg42930605 | 615 | TCTGCTTCTCTG<br>CCTCAGGCGG<br>CTC/TTCCTCCT<br>TCTCCAGCTCC<br>GTGGCCG      | C | T | Glu | Glu | SILENT-<br>CODING | struct | Human Gene Similar to SWISSPROT-<br>ID:P48788 TROPONIN I, FAST<br>SKELETAL MUSCLE (TROPONIN I,<br>FAST-TWITCH ISOFORM) - HOMO<br>SAPIENS (HUMAN), 181 aa.         | 1E-92   | 11<br>(11p15.5) |
| 428 | cg42930605 | 621 | TCTCTGCCTCAC<br>GGCGGCTCTCC<br>TC/C/TTCCTCCA<br>GCTCCGTGGCC<br>GCTATCT    | C | T | Lys | Lys | SILENT-<br>CODING | struct | Human Gene Similar to SWISSPROT-<br>ID:P48788 TROPONIN I, FAST<br>SKELETAL MUSCLE (TROPONIN I,<br>FAST-TWITCH ISOFORM) - HOMO<br>SAPIENS (HUMAN), 181 aa.         | 1E-92   | 11<br>(11p15.5) |
| 429 | cg42893961 | 51  | AATGGCCAGCA<br>GGAAGGCGGG<br>ACC/C/AJGGGC<br>AAGGTGGCAGC<br>CACCAAGCA     | C | A | Arg | Arg | SILENT-<br>CODING | struct | Human Gene Similar to SPTREMBL-<br>ID:Q01449 MYOSIN REGULATORY<br>LIGHT CHAIN, CARDIAC MUSCLE<br>ISOFORM - HOMO SAPIENS<br>(HUMAN), 175 aa.                       | 2.5E-89 |                 |
| 430 | cg42475816 | 282 | AATCAAGACAAA<br>CCCCAATTGAAA<br>A/G/AJAAAGATTG<br>AAGCCCCACTTTG<br>ATGCCA | G | A | Lys | Lys | SILENT-<br>CODING | struct | Human Gene Similar to SPTREMBL-<br>ID:Q10466 TITIN, HEART ISOFORM<br>N2-B (EC 2.7.1.-) (CONNECTIN) -<br>HOMO SAPIENS (HUMAN), 26926<br>aa.                        | 7.3E-85 | 2<br>(2q24.3)   |
| 431 | cg42522566 | 337 | TGAAGAACGTAA<br>AGGACCGGGAG<br>GA/T/CJGTGAAG<br>AATGAGGTCAA<br>CATCATGA   | T | C | Asp | Asp | SILENT-<br>CODING | struct | Human Gene Similar to SWISSPROT-<br>ID:P07313 MYOSIN LIGHT CHAIN<br>KINASE, SKELETAL MUSCLE (EC<br>2.7.1.117) (MLCK) - ORYCTOLAGUS<br>CUNICULUS (RABBIT), 607 aa. | 6E-55   |                 |

|     |            |     |  |   |   |     |     |                   |                      |  |          |    |
|-----|------------|-----|--|---|---|-----|-----|-------------------|----------------------|--|----------|----|
| 432 | cg43297806 | 953 | GTAGATGGGTA<br>GAATAGTAGCC<br>AGG[G/A]ACAAG<br>ACAGCGGTTCT<br>GCAGGGGAGC | G | A | Val | Val | SILENT-<br>CODING | sulfotran<br>sferase | Human Gene SWISSPROT-<br>ID:P52849 HEPARIN SULFATE N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE (EC 2.8.2.-)<br>(N- HSST) (N-HEPARIN SULFATE<br>SULFOTRANSFERASE)<br>(GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE) - HOMO<br>SAPIENS (HUMAN), 883<br>aa. pcis:TREMBLNEW-ID:G2792518<br>HEPARAN GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE-2 - HOMO<br>SAPIENS (HUMAN), 883 aa | 0.00E+00 | 10 |
| 433 | cg43297806 | 962 | TAGAATAGTAGC<br>CAGGGACAAGA<br>CA[G/A]CGGTTT<br>TGCAGGGAGCG<br>TAGTGCCA  | G | A | Arg | Arg | SILENT-<br>CODING | sulfotran<br>sferase | Human Gene SWISSPROT-<br>ID:P52849 HEPARIN SULFATE N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE (EC 2.8.2.-)<br>(N- HSST) (N-HEPARIN SULFATE<br>SULFOTRANSFERASE)<br>(GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE) - HOMO<br>SAPIENS (HUMAN), 883<br>aa. pcis:TREMBLNEW-ID:G2792518<br>HEPARAN GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE-2 - HOMO<br>SAPIENS (HUMAN), 883 aa | 0.00E+00 | 10 |





|     |            |      |   |   |   |     |     |                   |                      |  |          |    |
|-----|------------|------|---|---|---|-----|-----|-------------------|----------------------|--|----------|----|
| 436 | cg43297806 | 1016 | GGGCTGGGAG<br>GAGGCTGAAAT<br>CAC[C/T]TGATA<br>GAAGGTATAGTT<br>CAGAGCAA  | C | T | Gln | Gln | SILENT-<br>CODING | sulfotran<br>sferase | Human Gene SWISSPROT-<br>ID:P52849 HEPARIN SULFATE N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE (EC 2.8.2.-)<br>(N- HSST) (N-HEPARIN SULFATE<br>SULFOTRANSFERASE)<br>(GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE) - HOMO<br>SAPIENS (HUMAN), 883<br>aa. pcls:TREMBLNEW-ID:G2792518<br>HEPARAN GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE-2 - HOMO<br>SAPIENS (HUMAN), 883.aa | 0.00E+00 | 10 |
| 437 | cg43297806 | 1019 | TCTGGGAGGAG<br>GCTGAAATCAC<br>CTG[A/G]TAGAA<br>GGTATAGTTCAG<br>AGCAACTG | A | G | Tyr | Tyr | SILENT-<br>CODING | sulfotran<br>sferase | Human Gene SWISSPROT-<br>ID:P52849 HEPARIN SULFATE N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE (EC 2.8.2.-)<br>(N- HSST) (N-HEPARIN SULFATE<br>SULFOTRANSFERASE)<br>(GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE) - HOMO<br>SAPIENS (HUMAN), 883<br>aa. pcls:TREMBLNEW-ID:G2792518<br>HEPARAN GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE-2 - HOMO<br>SAPIENS (HUMAN), 883.aa | 0.00E+00 | 10 |

|     |            |      |   |   |   |     |     |                   |                      |  |          |    |
|-----|------------|------|---|---|---|-----|-----|-------------------|----------------------|--|----------|----|
| 438 | cg43297806 | 1028 | AGGCTGAAATC<br>ACCTGATAGAA<br>GGT[A/G]TAGTT<br>CAGAGCAACTG<br>GGTCTCCAT | A | G | Tyr | Tyr | SILENT-<br>CODING | sulfotran<br>sferase | Human Gene SWISSPROT-<br>ID:P52849 HEPARIN SULFATE N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE (EC 2.8.2.-)<br>(N- HSST) (N-HEPARIN SULFATE<br>SULFOTRANSFERASE)<br>(GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE) - HOMO<br>SAPIENS (HUMAN), 883<br>aa.lpcds:TREMBLNEW-ID:G2792518<br>HEPARAN GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE-2 - HOMO<br>SAPIENS (HUMAN), 883.aa | 0.00E+00 | 10 |
| 439 | cg43297806 | 1043 | GATAGAAGGTAT<br>AGTTCAGAGCA<br>ACT[A/GGGTCT<br>CCATGGGCTCG<br>CTGATGCT  | T | A | Pro | Pro | SILENT-<br>CODING | sulfotran<br>sferase | Human Gene SWISSPROT-<br>ID:P52849 HEPARIN SULFATE N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE (EC 2.8.2.-)<br>(N- HSST) (N-HEPARIN SULFATE<br>SULFOTRANSFERASE)<br>(GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE) - HOMO<br>SAPIENS (HUMAN), 883<br>aa.lpcds:TREMBLNEW-ID:G2792518<br>HEPARAN GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE-2 - HOMO<br>SAPIENS (HUMAN), 883.aa | 0.00E+00 | 10 |



|     |            |     |  |   |   |     |     |                   |          |  |          |  |
|-----|------------|-----|--|---|---|-----|-----|-------------------|----------|--|----------|--|
| 444 | cg39515668 | 655 | GGCGGAGCCCA<br>ACAAGGGCCAG<br>CAG[G]GCCCC<br>AGCAAGACCCT<br>CACCAGAGT    | G | C | Ala | Ala | SILENT-<br>CODING | synthase | Human Gene Similar to SWISSNEW-<br>ID:P54876<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE II (EC<br>6.3.5.3) (FGAM SYNTHASE II) -<br>MYCOBACTERIUM<br>TUBERCULOSIS, 754 aa. | 2.80E-72 |  |
| 445 | cg21428405 | 177 | TGACCTCGCCA<br>ATGACAGTGGC<br>AGC[G]AJACACC<br>CCAATGGGCGC<br>AGATCTCCA  | G | A | Val | Val | SILENT-<br>CODING | synthase | Human Gene Similar to SWISSNEW-<br>ID:P54876<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE II (EC<br>6.3.5.3) (FGAM SYNTHASE II) -<br>MYCOBACTERIUM<br>TUBERCULOSIS, 754 aa. | 2.20E-56 |  |
| 446 | cg21428405 | 273 | CCTGGGACTCG<br>CTCATGAGGAT<br>CTC[T]C]TCAGG<br>GGCGAGGTTCCG<br>GGTCGCGCA | T | C | Glu | Glu | SILENT-<br>CODING | synthase | Human Gene Similar to SWISSNEW-<br>ID:P54876<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE II (EC<br>6.3.5.3) (FGAM SYNTHASE II) -<br>MYCOBACTERIUM<br>TUBERCULOSIS, 754 aa. | 2.20E-56 |  |
| 447 | cg21428405 | 327 | GAACGCGGTCCG<br>AGCTCGACGTG<br>CAT[G]AJCCACC<br>GTCGCCAGCAC<br>TGGCCAGCT | G | A | Gly | Gly | SILENT-<br>CODING | synthase | Human Gene Similar to SWISSNEW-<br>ID:P54876<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE II (EC<br>6.3.5.3) (FGAM SYNTHASE II) -<br>MYCOBACTERIUM<br>TUBERCULOSIS, 754 aa. | 2.20E-56 |  |
| 448 | cg38924050 | 301 | TCTCGTTGATGA<br>GGTCGTTACCC<br>TC[A]G]CGGGTA<br>CGTTCACCGAC<br>ACCGCGGA  | A | G | Arg | Arg | SILENT-<br>CODING | synthase | Human Gene Similar to SWISSPROT-<br>ID:P50004 ATP SYNTHASE BETA<br>CHAIN (EC 3.6.1.34) -<br>STREPTOMYCES LIVIDANS, 477 aa.   | 2.60E-53 |  |
| 449 | cg38924050 | 310 | TGAGGTCGTTA<br>CCCTCACGGGT<br>ACG[T]C]TCACC<br>GACACCGGCGA<br>AAACCGAAG  | T | C | Glu | Glu | SILENT-<br>CODING | synthase | Human Gene Similar to SWISSPROT-<br>ID:P50004 ATP SYNTHASE BETA<br>CHAIN (EC 3.6.1.34) -<br>STREPTOMYCES LIVIDANS, 477 aa.   | 2.60E-53 |  |

|     |            |      |  |   |   |     |     |                   |          |  |           |    |
|-----|------------|------|--|---|---|-----|-----|-------------------|----------|--|-----------|----|
| 450 | cg38924050 | 352  | AAACCGAAGTA<br>CCGCCGAAGTT<br>GTG[G/C]GCGAT<br>ACGGTAAATCAT<br>CTCCTGAA  | G | C | Ala | Ala | SILENT-<br>CODING | synthase | Human Gene Similar to SWISSPROT-<br>ID:P50004 ATP SYNTHASE BETA<br>CHAIN (EC 3.6.1.34) -<br>STREPTOMYCES LIVIDANS, 477 aa. | 2.60E-53  |    |
| 451 | cg43925970 | 1703 | GAGCACATAAG<br>GTGAAGGTGGT<br>GAC[T/A]CCCAG<br>AGAAAGCGACCT<br>CTATATAGG | T | A | Gly | Gly | SILENT-<br>CODING | tm7      | Human Gene SPTREMBL-ID:O00348<br>PUTATIVE ENDOTHELIN<br>RECEPTOR TYPE B-LIKE PROTEIN -<br>HOMO SAPIENS (HUMAN), 613 aa.    | 0.00E+00  | 9  |
| 452 | cg41616031 | 1736 | AAGGGATGTCC<br>CCAAACTTCCAG<br>TC[T/C]GAACGC<br>CGCACATAGTA<br>GTCCATCA  | T | C | Ser | Ser | SILENT-<br>CODING | tm7      | Human Gene SWISSPROT-<br>ID:P49019 PROBABLE G PROTEIN-<br>COUPLED RECEPTOR HM74 -<br>HOMO SAPIENS (HUMAN), 387 aa.         | 2.90E-214 | 12 |
| 453 | cg41616031 | 1744 | TCCCCAAACTTC<br>CAGTCTGAACG<br>CC[G/T]CACATA<br>GTAGTCCATCAC<br>GAACGGC  | G | T | Arg | Arg | SILENT-<br>CODING | tm7      | Human Gene SWISSPROT-<br>ID:P49019 PROBABLE G PROTEIN-<br>COUPLED RECEPTOR HM74 -<br>HOMO SAPIENS (HUMAN), 387 aa.         | 2.90E-214 | 12 |
| 454 | cg41616031 | 1796 | GGCAGATGATC<br>AGTAGAAAGTCA<br>GC[T/C]ACTGCC<br>AGGTTGAACAG<br>GAAAAATCC | T | C | Val | Val | SILENT-<br>CODING | tm7      | Human Gene SWISSPROT-<br>ID:P49019 PROBABLE G PROTEIN-<br>COUPLED RECEPTOR HM74 -<br>HOMO SAPIENS (HUMAN), 387 aa.         | 2.90E-214 | 12 |



|     |            |     |   |   |   |     |     |                   |     |  |           |  |
|-----|------------|-----|---|---|---|-----|-----|-------------------|-----|--|-----------|--|
| 458 | cg42489842 | 432 | TTTGTGAGCAAAG<br>TTGATCAGTCTC<br>TTT/CATACCAA<br>CACATCGCTGG<br>ATGCTG  | T | C | Leu | Leu | SILENT-<br>CODING | tm7 | Human Gene Homologous to<br>SWISSPROT-ID:Q02038<br>NEUROLYSIN PRECURSOR (EC<br>3.4.24.16) (NEUROTENSIN<br>ENDOPEPTIDASE)<br>(MITOCHONDRIAL<br>OLIGOPEPTIDASE M)<br>(MICROSOMAL ENDOPEPTIDASE)<br>(MEP) (SOLUBLE ANGIOTENSIN-<br>BINDING PROTEIN) (SABP) - SUS<br>SCROFA (PIG), 704 aa. | 7.30E-106 |  |
| 459 | cg42489842 | 456 | TTCATACCAACA<br>CATCGCTGGAT<br>GCTT/CJGCAAGT<br>GAATATGCCAAA<br>TACTGCT | T | C | Ala | Ala | SILENT-<br>CODING | tm7 | Human Gene Homologous to<br>SWISSPROT-ID:Q02038<br>NEUROLYSIN PRECURSOR (EC<br>3.4.24.16) (NEUROTENSIN<br>ENDOPEPTIDASE)<br>(MITOCHONDRIAL<br>OLIGOPEPTIDASE M)<br>(MICROSOMAL ENDOPEPTIDASE)<br>(MEP) (SOLUBLE ANGIOTENSIN-<br>BINDING PROTEIN) (SABP) - SUS<br>SCROFA (PIG), 704 aa. | 7.30E-106 |  |
| 460 | cg42489842 | 471 | CGCTGGATGCT<br>GCAAGTGAATAT<br>GC/C/TJAAATACT<br>GCTCAGAAATAT<br>TAGGAG | C | T | Ala | Ala | SILENT-<br>CODING | tm7 | Human Gene Homologous to<br>SWISSPROT-ID:Q02038<br>NEUROLYSIN PRECURSOR (EC<br>3.4.24.16) (NEUROTENSIN<br>ENDOPEPTIDASE)<br>(MITOCHONDRIAL<br>OLIGOPEPTIDASE M)<br>(MICROSOMAL ENDOPEPTIDASE)<br>(MEP) (SOLUBLE ANGIOTENSIN-<br>BINDING PROTEIN) (SABP) - SUS<br>SCROFA (PIG), 704 aa. | 7.30E-106 |  |
| 461 | cg42927358 | 947 | TTTGTCTTTGC<br>CAACATCATCC<br>T[G/A]ACAAATG<br>GTCAGCCAACA<br>GAGGACA   | G | A | Leu | Leu | SILENT-<br>CODING | tm7 | Human Gene Similar to SWISSPROT-<br>ID:Q15391 PROBABLE G PROTEIN-<br>COUPLED RECEPTOR KIAA0001 -<br>HOMO SAPIENS (HUMAN), 338 aa.  | 1.40E-71  |  |



|     |            |      |   |   |   |     |     |                   |                      |  |           |          |
|-----|------------|------|---|---|---|-----|-----|-------------------|----------------------|--|-----------|----------|
| 462 | cg42927358 | 544  | ATGAATTGACA<br>CAATTGCTTGC<br>C[G/A]GTGCTTT<br>ATCTCATTATAT<br>TTGTGG   | G | A | Pro | Pro | SILENT-<br>CODING | tm7                  | Human Gene Similar to SWISSPROT-<br>ID:Q15391 PROBABLE G PROTEIN-<br>COUPLED RECEPTOR KIAA0001 -<br>HOMO SAPIENS (HUMAN), 338 aa.  | 1.40E-71  |          |
| 463 | cg32423505 | 1056 | CCCTCCTCCTG<br>GCTGAGAAAA<br>GTT[G/T]CCCTT<br>GTGCAAAAAACA<br>CTAGGTACC | G | T | Gly | Gly | SILENT-<br>CODING | tm7                  | Human Gene Similar to SPTREMBL-<br>ID:Q89609 G PROTEIN-COUPLED<br>RECEPTOR - EQUINE<br>HERPESVIRUS TYPE 2 (EHV-2), 383<br>aa.  | 1.20E-55  | 3 (3q21) |
| 464 | cg43968711 | 2389 | TATGATTGGATG<br>TGGAAGAACTAT<br>C[T/C]GTTGCATT<br>CACATTTAAACG<br>ATTGG | T | C | Thr | Thr | SILENT-<br>CODING | transcript<br>factor | Human Gene SWISSPROT-<br>ID:P32780 BASIC TRANSCRIPTION<br>FACTOR 62 KD SUBUNIT (P62) -<br>HOMO SAPIENS (HUMAN), 548 aa.  | 2.30E-292 | 11       |
| 465 | cg43297259 | 800  | CTCCTGTGTGT<br>GTCCTTAAGTGT<br>CT[G/A]ATGAGG<br>TGTGACTTCTGG<br>CTAAAGC | G | A | Ile | Ile | SILENT-<br>CODING | transcript<br>factor | Human Gene Similar to SWISSNEW-<br>ID:Q61751 RENAL TRANSCRIPTION<br>FACTOR KID-1 (TRANSCRIPTION<br>FACTOR 17) - MUS MUSCULUS<br>(MOUSE), 572 aa   pcds:SWISSPROT-<br>ID:Q61751 RENAL TRANSCRIPTION<br>FACTOR KID-1 (TRANSCRIPTION<br>FACTOR 17) - MUS MUSCULUS<br>(MOUSE), 572 aa. | 7.80E-54  |          |
| 466 | cg20612302 | 301  | TGGAGGCGGCC<br>CACATGGCGGC<br>CAC[C/G]GCCAT<br>CCTCAACCTGTC<br>CACGCGCT | C | G | Thr | Thr | SILENT-<br>CODING | transcript<br>factor | Human Gene Similar to SPTREMBL-<br>ID:O08996 MYELIN<br>TRANSCRIPTION FACTOR 1-LIKE -<br>MUS MUSCULUS (MOUSE), 1182<br>aa.  | 1.70E-53  |          |
| 467 | cg43949162 | 856  | GGGCCATGTTA<br>ACCACTTCCTTT<br>TG[C/T]TGATCAT<br>CTGGTTTAAAGA<br>AAGGAT | C | T | Gln | Gln | SILENT-<br>CODING | transferase          | Human Gene Homologous to<br>TREMBLNEW-ID:G2738933<br>GLUTATHIONE TRANSFERASE (EC<br>2.5.1.18) - HOMO SAPIENS<br>(HUMAN), 222 aa.   | 1.30E-115 | 6        |

|     |            |      |  |   |   |     |     |                   |             |   |           |   |
|-----|------------|------|--|---|---|-----|-----|-------------------|-------------|---|-----------|---|
| 468 | cg43928442 | 449  | CATCCACATGG<br>GCCACGGTGAT<br>GGG[C/A]AGCCC<br>AAAGGCTCCGT<br>ATCTGCAGG  | C | A | Leu | Leu | SILENT-<br>CODING | transferase | Human Gene Similar to SPTREMBL-ID:O09034 GLUTATHIONE S-TRANSFERASE SUBUNIT 13 - RATTUS NORVEGICUS (RAT), 226 aa.  | 2.60E-87  | 7 |
| 469 | cg43976701 | 1859 | GACAGCTCATTC<br>GACTGTGTCAG<br>AA[A/G]TTTGA<br>GAATATCATAAA<br>GATGACC   | A | G | Lys | Lys | SILENT-<br>CODING | transport   | Human Gene SWISSPROT-ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa.  | 0.00E+00  |   |
| 470 | cg44005525 | 975  | CTTGACTGTTAA<br>TATTACAATGAT<br>A[G/A]ATTCCTGT<br>CCGAAATGTAAC<br>CTTTG  | G | A | Ile | Ile | SILENT-<br>CODING | ubiquitin   | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |   |
| 471 | cg44005525 | 1041 | ATTCTGGTGTA<br>AAGTGATATCGA<br>G[A/G]AAGAATA<br>CACACCCCTCAT<br>ACACGG   | A | G | Phe | Phe | SILENT-<br>CODING | ubiquitin   | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |   |
| 472 | cg44005525 | 1047 | GTGTAAAAGTGA<br>TATCGAGAAAGA<br>AT[G/A]ACACAC<br>CCTCATACACG<br>GATCCTG  | T | G | Val | Val | SILENT-<br>CODING | ubiquitin   | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |   |
| 473 | cg44005525 | 1065 | GAAAGAATACAC<br>CACCCCTCATACA<br>C[G/A]GATCCTG<br>GAGGCCCTAGA<br>ATGGTTG | G | A | Ser | Ser | SILENT-<br>CODING | ubiquitin   | Human Gene Homologous to SWISSPROT-ID:P51965 UBIQUITIN-CONJUGATING ENZYME E2-21 KD UBCH6 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 193 aa. | 3.30E-101 |   |

|     |            |      |   |   |   |     |     |                   |           |   |           |  |
|-----|------------|------|---|---|---|-----|-----|-------------------|-----------|---|-----------|--|
| 474 | cg44005525 | 1080 | CCTCATACACG<br>GATCTGGAGG<br>CCCT/CJAGAAT<br>GGTTGATCTCCA<br>TTCATAGA     | T | C | Leu | Leu | SILENT-<br>CODING | ubiquitin | Human Gene Homologous to<br>SWISSPROT-ID:P51965 UBIQUITIN-<br>CONJUGATING ENZYME E2-21 KD<br>UBCH6 (EC 6.3.2.19) (UBIQUITIN-<br>PROTEIN LIGASE) (UBIQUITIN<br>CARRIER PROTEIN) - HOMO<br>SAPIENS (HUMAN), 193 aa. | 3.30E-101 |  |
| 475 | cg44005525 | 1098 | GAGGCCCTAGA<br>ATGGTTGATCTC<br>CAIT/CJTCATAGA<br>TGTTATCGCCTT<br>TGGGAC   | T | C | Glu | Glu | SILENT-<br>CODING | ubiquitin | Human Gene Homologous to<br>SWISSPROT-ID:P51965 UBIQUITIN-<br>CONJUGATING ENZYME E2-21 KD<br>UBCH6 (EC 6.3.2.19) (UBIQUITIN-<br>PROTEIN LIGASE) (UBIQUITIN<br>CARRIER PROTEIN) - HOMO<br>SAPIENS (HUMAN), 193 aa. | 3.30E-101 |  |
| 476 | cg44005525 | 1110 | TGGTTGATCTCC<br>ATTTCATAGATGT<br>TIA/GJTCGCCTTT<br>GGGACCAGCAC<br>TGCAAT  | A | G | Asp | Asp | SILENT-<br>CODING | ubiquitin | Human Gene Homologous to<br>SWISSPROT-ID:P51965 UBIQUITIN-<br>CONJUGATING ENZYME E2-21 KD<br>UBCH6 (EC 6.3.2.19) (UBIQUITIN-<br>PROTEIN LIGASE) (UBIQUITIN<br>CARRIER PROTEIN) - HOMO<br>SAPIENS (HUMAN), 193 aa. | 3.30E-101 |  |
| 477 | cg44005525 | 1134 | TATCGCCCTTTGG<br>GACCAGCACTG<br>CAIA/GJTtagGT<br>GGAGGGTCTAA<br>AGTGAITGT | A | G | Asn | Asn | SILENT-<br>CODING | ubiquitin | Human Gene Homologous to<br>SWISSPROT-ID:P51965 UBIQUITIN-<br>CONJUGATING ENZYME E2-21 KD<br>UBCH6 (EC 6.3.2.19) (UBIQUITIN-<br>PROTEIN LIGASE) (UBIQUITIN<br>CARRIER PROTEIN) - HOMO<br>SAPIENS (HUMAN), 193 aa. | 3.30E-101 |  |
| 478 | cg44005525 | 828  | TGTTGGTCATAT<br>ACTGAGTGGCA<br>ATIA/GJCTTCCC<br>ACCAAAGGGTC<br>GGCAGGAT   | A | G | Ser | Ser | SILENT-<br>CODING | ubiquitin | Human Gene Homologous to<br>SWISSPROT-ID:P51965 UBIQUITIN-<br>CONJUGATING ENZYME E2-21 KD<br>UBCH6 (EC 6.3.2.19) (UBIQUITIN-<br>PROTEIN LIGASE) (UBIQUITIN<br>CARRIER PROTEIN) - HOMO<br>SAPIENS (HUMAN), 193 aa. | 3.30E-101 |  |

|     |            |      |   |   |   |     |                   |                  |  |          |                      |
|-----|------------|------|---|---|---|-----|-------------------|------------------|--|----------|----------------------|
| 479 | cg17663981 | 225  | CCGAGAACCCG<br>GGCACAGCGAG<br>AGC[C/G]TGGTG<br>CCAAGTGGCCC<br>AAAAGTTCA | C | G | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:Q05329 GLUTAMATE<br>DECARBOXYLASE, 65 KD<br>ISOFORM (EC 4.1.1.15) (GAD-65)<br>(65 KD GLUTAMIC ACID<br>DECARBOXYLASE) - Homo sapiens<br>(Human), 585 aa. | 0.00E+00 | 10<br>(10p11.2<br>3) |
| 480 | cg17663981 | 234  | CGGGCACAGCG<br>AGAGCCTGGTG<br>CCA[A/G]GTGGC<br>CCAAAAGTTTAC<br>GGCGGGCA | A | G | Gln | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:Q05329 GLUTAMATE<br>DECARBOXYLASE, 65 KD<br>ISOFORM (EC 4.1.1.15) (GAD-65)<br>(65 KD GLUTAMIC ACID<br>DECARBOXYLASE) - Homo sapiens<br>(Human), 585 aa. | 0.00E+00 | 10<br>(10p11.2<br>3) |
| 481 | cg42907760 | 1501 | AACCTGAAGGC<br>CAAAAGTTTGAC<br>TC[G/A]GACTCG<br>GAGAGCACAGT<br>CAGCCCCC | G | A | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q15464 SHB MRNA - HOMO<br>SAPIENS (HUMAN), 596 aa.   | 0.00E+00 | 9 (9p12)             |
| 482 | cg43301812 | 3795 | CTCCATGGCTG<br>GGATGCTCTGC<br>TGC[G/A]CTTGG<br>TTTTGCCCGAGT<br>GGCAGCCT | G | A | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:Q93075 HYPOTHETICAL<br>PROTEIN KIAA0218 - Homo sapiens<br>(Human), 761 aa.  | 0.00E+00 | 3                    |
| 483 | cg43917756 | 1098 | AGACACTGACC<br>ACTGGGGGAGG<br>TGC[A/G]GAGAC<br>TGTGCTGGATG<br>TGGTGGAAA | A | G | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:Q14157 HYPOTHETICAL<br>PROTEIN KIAA0144 - Homo sapiens<br>(Human), 983 aa.  | 0.00E+00 | 1                    |
| 484 | cg43918356 | 2645 | CATCTTCATCTA<br>GAAACGCCCTC<br>AC[G/T]GAAATG<br>GAATTGCTGCC<br>AGACGTGG | G | T | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75176 KIAA0692 PROTEIN -<br>HOMO SAPIENS (HUMAN), 783 aa<br>(fragment).   | 0.00E+00 | 12                   |



|     |            |      |  |   |   |     |                   |                  |   |          |   |
|-----|------------|------|--|---|---|-----|-------------------|------------------|---|----------|---|
| 491 | cg43999667 | 3688 | GTACAGCCTGG<br>TAATGGAGAATC<br>AA[A/G]TTTGTCT<br>GTATCGTAAAG<br>GCAGCAA  | A | G | Asn | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O60281 KIAA0530 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1563 aa<br>(fragment).   | 0.00E+00 | 6 |
| 492 | cg44009187 | 6789 | TCAACTTGCTCC<br>AGTAGGCCGCC<br>GG[C/T]TCTGCA<br>GGCAGCTCGGG<br>CTGGAAGA  | C | T | Glu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P42858 HUNTINGTIN<br>(HUNTINGTON'S DISEASE<br>PROTEIN) (HD PROTEIN) - Homo<br>sapiens (Human), 3144 aa.                        | 0.00E+00 |   |
| 493 | cg44020180 | 3172 | ATGGGTAGACT<br>CGAGTTTGGTAA<br>AT[G/A]TCCAAA<br>CCATAGGCCAC<br>AACCAAAC  | G | A | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00 | 1 |
| 494 | cg44020180 | 3177 | TAGACTCGAGTT<br>TGGTAAATGTCC<br>A[A/G]ACCATAG<br>GCCACAACCAA<br>ACAAAGTG | A | G | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00 | 1 |
| 495 | cg44020180 | 3199 | CCAAACCATAG<br>GCCACAACCAA<br>ACA[A/T]GTGGA<br>CTCCAGACCCG<br>AGGGAGCTG  | A | T | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00 | 1 |
| 496 | cg44020180 | 3211 | CCACAACCAA<br>CAAGTGGAATC<br>CAG[A/G]CCCCGA<br>GGGAGCTGTGT<br>AGATACCTC  | A | G | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00 | 1 |

|     |            |      |   |   |   |     |     |                   |                  |   |          |   |
|-----|------------|------|---|---|---|-----|-----|-------------------|------------------|---|----------|---|
| 497 | cg44020180 | 3220 | AACAAGTGGAC<br>TCCAGACCCGA<br>GGG[A/C]GCTGT<br>GTAGATACCTC<br>GCATTCGAG | A | C | Ala | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00 | 1 |
| 498 | cg44020180 | 3226 | TGGACTCCAGA<br>CCCGAGGGAGC<br>TGT[G/A]TAGATA<br>CCTCGCATTCG<br>AGAAACTG | G | A | Tyr | Tyr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00 | 1 |
| 499 | cg44020180 | 3232 | CCAGACCCGAG<br>GGAGCTGTGTA<br>GAT[G/C]CCTCG<br>CATTGAGAAAC<br>TGCTGGT   | A | G | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00 | 1 |
| 500 | cg44020180 | 3247 | CTGTGTAGATAC<br>CTCGCATTCGA<br>GA[A/G]ACTGTC<br>TGGTTATAGTTG<br>ATGAATC | A | G | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00 | 1 |
| 501 | cg44020180 | 3289 | TGATGAATCGCT<br>CTGCGTGTATCT<br>GT[G]ACATCTG<br>GAGAATACGGG<br>ATTAAGT  | T | G | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00 | 1 |
| 502 | cg44020180 | 3298 | GCTCTGCGTGT<br>ATCTGTACATCT<br>GG[A/G]GAATAC<br>GGGATTAAGTTC<br>TCCTCTC | A | G | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00 | 1 |

|     |            |      |  |   |   |     |     |                   |                  |   |           |                     |
|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|---|-----------|---------------------|
| 503 | cg44020180 | 3312 | TGTACATCTGGA<br>GAATACGGGAT<br>TA[A/G]GTTCTC<br>CTCTCTGCTTTG<br>TTCTGTT  | A | G | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00  | 1                   |
| 504 | cg44020180 | 3319 | CTGGAGAATAC<br>GGGATTAAGTTC<br>TC[C/T]TCTCTGC<br>TTTGTTCTGTTG<br>GGATCT  | C | T | Glu | Glu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14700 MRNA (KIAA0090) FOR<br>ORF (RELATED TO YEAST GENE IN<br>CHROMOSOME III) - HOMO<br>SAPIENS (HUMAN), 905 aa<br>(fragment). | 0.00E+00  | 1                   |
| 505 | cg44928323 | 2080 | AGCAGGCAGAT<br>AGAAGTTCCTGT<br>CA[C/T]TTTCTCC<br>TTTTTACGGGG<br>TAGGAT   | C | T | His | His | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:P97526 NEUROFIBROMIN -<br>RATTUS NORVEGICUS (RAT), 2820<br>aa.  | 0.00E+00  | 17<br>(17q11.2<br>) |
| 506 | cg44932392 | 1281 | TGCTTTGGTTTT<br>TGATAAAATTGT<br>T[G/A]AACTTATT<br>GTTGAGATCAG<br>CGCTGA  | G | A | Phe | Phe | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD23581 CULLIN 2 - HOMO<br>SAPIENS (HUMAN), 745 aa.   | 0.00E+00  |                     |
| 507 | cg43991434 | 1266 | TCTTGAGCAGA<br>CCCATGTGCAC<br>GAG[G/C]AGCCT<br>GGTGAGGAAGG<br>TGTTGGAGT  | G | C | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:P46060 RAN-GTPASE<br>ACTIVATING PROTEIN 1 - Homo<br>sapiens (Human), 587 aa.  | 1.70E-304 | 22                  |
| 508 | cg43985955 | 1994 | GCATGATAGGA<br>TATGGAATTCCT<br>CC[A/T]CAAAATG<br>GGAAGTGTTCC<br>TGTAATGA | A | T | Pro | Pro | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13492 CALM (TYPE I CALM<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 652 aa.   | 2.70E-299 |                     |
| 509 | cg43985955 | 2009 | GAATTCCTCCAC<br>AAATGGGAAGT<br>GTT[A/C]CTGTAA<br>TGACGCAACCA<br>ACCTTAA  | T | A | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13492 CALM (TYPE I CALM<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 652 aa.   | 2.70E-299 |                     |



|     |            |      |  |   |   |     |     |                   |                  |   |           |    |
|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|---|-----------|----|
| 510 | cg43985955 | 2021 | AAATGGGAAGT<br>GTTCCCTGTAATG<br>AC[G/A]CAACCA<br>ACCTTAATATAC<br>AGCCAGC | G | A | Thr | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13492 CALM (TYPE I CALM<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 652 aa.   | 2.70E-299 |    |
| 511 | cg43985955 | 2060 | TATACAGCCAG<br>CCTGTCATGAG<br>ACC[T/G]CCAAA<br>CCCCTTTGGCC<br>CTGTATCAG  | T | G | Pro | Pro | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13492 CALM (TYPE I CALM<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 652 aa.   | 2.70E-299 |    |
| 512 | cg44031765 | 2070 | ACCTCGCCGTA<br>GTAGATGTAGC<br>GCA[G/A]CATGG<br>ACTCGAAGGCC<br>TGCCTGCTG  | G | A | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14776 LZTR-1 - HOMO<br>SAPIENS (HUMAN), 552 aa.  | 4.60E-279 | 22 |
| 513 | cg43252100 | 466  | TGCAGCCCGA<br>GGTTCCTTTTAC<br>TC[C/A]ATGGTA<br>CCAAATGCAACT<br>ATTACAC   | C | A | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA83037 KIAA1085 PROTEIN -<br>HOMO SAPIENS (HUMAN), 584 aa<br>(fragment).                                     | 4.90E-278 |    |
| 514 | cg43934178 | 2445 | CGATGCCATGC<br>TTCTCCATGAGC<br>GT[G/A]ATGAGC<br>TCGGCCTCCGT<br>CAGGTAGT  | G | A | Ile | Ile | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD29670 DNA<br>TOPOISOMERASE III BETA - HOMO<br>SAPIENS (HUMAN), 862 aa.                                      | 1.80E-274 |    |
| 515 | cg43031103 | 1696 | ACATGGCCCTC<br>CCCTTGGTTGA<br>GGA[G/A]ACAGC<br>AGGGGCTGGTG<br>TGAGGTGCA  | G | A | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O60240 PERILIPIN - HOMO<br>SAPIENS (HUMAN), 522 aa.   | 6.30E-266 |    |
| 516 | cg43258841 | 340  | TAAATCTTGTGT<br>GGCCATCATCC<br>AG[T/G]GTGTGG<br>AACATTTACCCG<br>TCATCTT  | T | G | Thr | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q14449 GROWTH FACTOR<br>RECEPTOR-BOUND PROTEIN 14<br>(GRB14 ADAPTER PROTEIN) -<br>Homo sapiens (Human), 540 aa. | 2.70E-258 |    |

|     |            |     |  |   |   |     |     |                   |                  |   |           |  |
|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|---|-----------|--|
| 517 | cg43258841 | 358 | CATCCAGTGTGT<br>GGAACATTTTCAC<br>C[G/A]TCATCTTC<br>TACTGGTATAAT<br>TTGAA | G | A | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q14449 GROWTH FACTOR<br>RECEPTOR-BOUND PROTEIN 14<br>(GRB14 ADAPTER PROTEIN) -<br>Homo sapiens (Human), 540 aa. | 2.70E-258 |  |
| 518 | cg43258841 | 370 | GGAACATTTTCAC<br>CGTCATCTTCTA<br>C[T/G]GGTATAA<br>TTTGAAAGTGCT<br>TTATTT | T | G | Pro | Pro | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q14449 GROWTH FACTOR<br>RECEPTOR-BOUND PROTEIN 14<br>(GRB14 ADAPTER PROTEIN) -<br>Homo sapiens (Human), 540 aa. | 2.70E-258 |  |
| 519 | cg43258841 | 388 | CTTCTACTGGTA<br>TAATTTGAAAGT<br>G[C/T]TTTATTT<br>TTGTCCATGACT<br>CATTG   | C | T | Lys | Lys | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q14449 GROWTH FACTOR<br>RECEPTOR-BOUND PROTEIN 14<br>(GRB14 ADAPTER PROTEIN) -<br>Homo sapiens (Human), 540 aa. | 2.70E-258 |  |
| 520 | cg43258841 | 394 | CTGGTATAATTT<br>GAAAGTGCTTTA<br>T[T/C]TTTTGTCC<br>ATGACTCATTGA<br>CAGTA  | T | C | Lys | Lys | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q14449 GROWTH FACTOR<br>RECEPTOR-BOUND PROTEIN 14<br>(GRB14 ADAPTER PROTEIN) -<br>Homo sapiens (Human), 540 aa. | 2.70E-258 |  |
| 521 | cg43258841 | 403 | TTTGAAAGTGCT<br>TTATTTTTTGTC<br>C[A/G]TGACTCA<br>TTGACAGTACGA<br>AAGTTT  | A | G | His | His | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q14449 GROWTH FACTOR<br>RECEPTOR-BOUND PROTEIN 14<br>(GRB14 ADAPTER PROTEIN) -<br>Homo sapiens (Human), 540 aa. | 2.70E-258 |  |
| 522 | cg43258841 | 421 | TTTGTCCATGAC<br>TCATTGACAGTA<br>C[G/A]AAAGTTTT<br>GGGGTTACTCT<br>GACTAT  | G | A | Phe | Phe | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q14449 GROWTH FACTOR<br>RECEPTOR-BOUND PROTEIN 14<br>(GRB14 ADAPTER PROTEIN) -<br>Homo sapiens (Human), 540 aa. | 2.70E-258 |  |
| 523 | cg43258841 | 484 | AAACTCCATCCA<br>CAAGTCCTTGCT<br>G[A/G]ATAATCA<br>ATCGCTGAGCC<br>TCATCTC  | A | G | Ile | Ile | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q14449 GROWTH FACTOR<br>RECEPTOR-BOUND PROTEIN 14<br>(GRB14 ADAPTER PROTEIN) -<br>Homo sapiens (Human), 540 aa. | 2.70E-258 |  |
| 524 | cg43258841 | 493 | CCACAAGTCCTT<br>GCTGAATAATCA<br>A[T/C]CGCTGAG<br>CCTCATCTCTAG<br>AAATTT  | T | C | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q14449 GROWTH FACTOR<br>RECEPTOR-BOUND PROTEIN 14<br>(GRB14 ADAPTER PROTEIN) -<br>Homo sapiens (Human), 540 aa. | 2.70E-258 |  |



|     |            |      |   |   |   |     |     |                   |                  |  |           |                 |
|-----|------------|------|---|---|---|-----|-----|-------------------|------------------|--|-----------|-----------------|
| 532 | cg42676981 | 1712 | GGAAGTAGAGG<br>TCAGGTGGGC<br>TGT[G]AGGCT<br>CTTCAGGTTCAA<br>ACACCGGA    | G | A | Pro | Pro | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P08910 PROTEIN PHPS1-2 -<br>Homo sapiens (Human), 425 aa.   | 5.90E-231 | 15              |
| 533 | cg43918561 | 843  | GGAAGGAGGTC<br>TACACCACGCT<br>GAA[G]AGGCT<br>CTACGCCACGC<br>ACGCCTGCG   | G | A | Lys | Lys | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P04177 TYROSINE 3-<br>MONOOXYGENASE (EC 1.14.16.2)<br>(TYROSINE 3-HYDROXYLASE) (TH)<br>Rattus norvegicus (Rat), 498 aa. | 2.10E-224 | 11<br>(11p15.5) |
| 534 | cg43999712 | 566  | ACGTACCAAATG<br>AAATGCTCTACG<br>G[G]CJCGAATAG<br>GCTACATCTATG<br>CTCTGC | G | C | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O43813<br>SEVENTRANSMEMBRANE-DOMAIN<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 399 aa.  | 3.30E-221 | 2               |
| 535 | cg43999712 | 569  | TACCAAATGAAA<br>TGCTCTACGGG<br>CG[A]CJATAGGC<br>TACATCTATGCT<br>CTGCTTT | A | C | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O43813<br>SEVENTRANSMEMBRANE-DOMAIN<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 399 aa.  | 3.30E-221 | 2               |
| 536 | cg43999712 | 659  | GCCATATTCAGC<br>AGATTTGTGAAA<br>C[A]CJATTTTAAC<br>CTCTGGAGAAA<br>ACCTAT | A | C | Thr | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O43813<br>SEVENTRANSMEMBRANE-DOMAIN<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 399 aa.  | 3.30E-221 | 2               |
| 537 | cg43922139 | 1860 | ACTTGACTTTCC<br>AGACACGGTGA<br>GG[A]GJAGGAGG<br>AGGCTGTCGGG<br>ACCAAACG | A | G | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O88473 RJS - MUS<br>MUSCULUS (MOUSE), 4836 aa.   | 2.80E-218 |                 |
| 538 | cg43955639 | 512  | CAGGCATGGTG<br>ATGAGGGGTGC<br>TGG[G/T]GCCAG<br>GGAGGTGGCAG<br>GAGCTGGCA | G | T | Ala | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O15417 CAGL79 - HOMO<br>SAPIENS (HUMAN), 413 aa<br>(fragment).   | 2.80E-215 |                 |



|     |            |      |   |   |   |     |     |                   |                  |  |           |                    |
|-----|------------|------|---|---|---|-----|-----|-------------------|------------------|--|-----------|--------------------|
| 546 | cg43918701 | 1667 | TTTTCCAGATGC<br>GACAGACATCAT<br>TTT/CJGGGCATA<br>TTCTAGAAACCA<br>AGGGCA   | T | C | Pro | Pro | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O60736 KE03 PROTEIN -<br>HOMO SAPIENS (HUMAN), 367 aa<br>(fragment).   | 1.10E-170 |                    |
| 547 | cg43926685 | 815  | AGAATTCCTTAC<br>TGGATCACCGC<br>AA[C/T]AAGACC<br>ATCCACAACGAT<br>TACCGCA   | C | T | Asn | Asn | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:P23280 CARBONIC<br>ANHYDRASE VI PRECURSOR (EC<br>4.2.1.1) (CARBONATE<br>DEHYDRATASE VI) - Homo sapiens<br>(Human), 308 aa. | 2.50E-168 | 1<br>(1p36.33<br>) |
| 548 | cg44927654 | 263  | GTGCCAGCTTC<br>TCCATGGTGGC<br>ATC[C/T]GTCAG<br>GATGCTGGGT<br>AGGGAGGTT    | C | T | Thr | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA74865 KIAA0842 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1020 aa<br>(fragment).   | 7.3E-165  |                    |
| 549 | cg43993462 | 2019 | CCAACTCATTGA<br>CAGTGAGGGGT<br>GC[G/A]TCTCCA<br>CTTCTGTTGGTG<br>TAATTGA   | G | A | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q63965 TRICARBOXYLATE<br>CARRIER - RATTUS NORVEGICUS<br>(RAT), 357 aa (fragment).  | 5.1E-161  | 5                  |
| 550 | cg44010310 | 1180 | CTATATTCTCTG<br>ATTGTGCAAAAGT<br>A[C/T]AGGACAT<br>TATATTCGACAT<br>CTTTGG  | C | T | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA32101 BCAP - HOMO<br>SAPIENS (HUMAN), 331 aa.  | 1.3E-155  | 13                 |
| 551 | cg43950590 | 1319 | GGTGCAACCATG<br>TACAGCTGCCC<br>AAT[C/T]TGAGA<br>GAAGAATCCTC<br>CGACGGGCTT | C | T | Gln | Gln | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75323 GBAS - HOMO<br>SAPIENS (HUMAN), 286 aa.   | 1.9E-154  | 7                  |
| 552 | cg43950590 | 1334 | GCTGCCCAATC<br>TGAGAGAAGAA<br>TCC[T/C]CCGAC<br>GGCTTCGTTAC<br>CATCCTGTC   | T | C | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75323 GBAS - HOMO<br>SAPIENS (HUMAN), 286 aa.   | 1.90E-154 | 7                  |

|     |            |      |  |   |   |     |     |                   |                  |   |           |    |
|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|---|-----------|----|
| 553 | cg43950590 | 1361 | CGACGGCTTCG<br>TTACCATCCTGT<br>CT[G/A]AAGCGG<br>ATTGCACGAGC<br>CCAGTAAT  | G | A | Phe | Phe | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75323 GBAS - HOMO<br>SAPIENS (HUMAN), 286 aa.                    | 1.90E-154 | 7  |
| 554 | cg43950590 | 1370 | CGTTACCATCCT<br>GTCTGAAGCGG<br>ATT[G/G]GCACGA<br>GCCAGTAATT<br>GCCCCATT  | T | G | Ala | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75323 GBAS - HOMO<br>SAPIENS (HUMAN), 286 aa.                    | 1.90E-154 | 7  |
| 555 | cg43950590 | 1376 | CATCCTGTCTGA<br>AGCGGATTGCA<br>CG[A/G]GCCCGAG<br>TAATTGCCCCAT<br>TCAATCA | A | G | Ala | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75323 GBAS - HOMO<br>SAPIENS (HUMAN), 286 aa.                    | 1.90E-154 | 7  |
| 556 | cg43950590 | 1397 | CACGAGCCCGAG<br>TAATTGCCCCAT<br>TC[A/G]ATCATG<br>GTTCTTGGTCG<br>GAGTTGGT | A | G | Ile | Ile | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75323 GBAS - HOMO<br>SAPIENS (HUMAN), 286 aa.                    | 1.90E-154 | 7  |
| 557 | cg43950590 | 1436 | GTCGGAGTTGG<br>TAAGACCTGAGT<br>TC[A/G]TATATAT<br>TAGGTCCGGAT<br>CTTGGCA  | A | G | Tyr | Tyr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75323 GBAS - HOMO<br>SAPIENS (HUMAN), 286 aa.                    | 1.90E-154 | 7  |
| 558 | cg43950590 | 1445 | GGTAAGACCTG<br>AGTTCATATATA<br>TT[A/G]GGTCCG<br>GATCTTGGCAC<br>AGGCTCAT  | A | G | Pro | Pro | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75323 GBAS - HOMO<br>SAPIENS (HUMAN), 286 aa.                    | 1.90E-154 | 7  |
| 559 | cg43951092 | 1484 | GAGTAGAATTCA<br>AGAAGAGTTCAA<br>TTA/GTATCGAT<br>GTTGCATGTTAT<br>TTTTAT   | A | G | Tyr | Tyr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD45179<br>RIBONUCLEOPROTEIN - HOMO<br>SAPIENS (HUMAN), 346 aa. | 4.50E-152 | 14 |

|     |            |      |  |   |   |     |     |                   |                  |   |           |    |
|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|---|-----------|----|
| 560 | cg43951092 | 1526 | TATTTTATCTTT<br>AGACATGGCAG<br>CTT/CJACTGCAT<br>CTTCATGTGTCA<br>CAAACT   | T | C | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD45179<br>RIBONUCLEOPROTEIN - HOMO<br>SAPIENS (HUMAN), 346 aa.                             | 4.50E-152 | 14 |
| 561 | cg43951092 | 1583 | CTGCTTCTCCTG<br>TGCTCTGCTGCA<br>TC[A/G]GCTCCA<br>ATATCAATATGA<br>ACTCGTA | A | G | Ala | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD45179<br>RIBONUCLEOPROTEIN - HOMO<br>SAPIENS (HUMAN), 346 aa.                             | 4.50E-152 | 14 |
| 562 | cg43951092 | 1604 | CATCAGCTCCAA<br>TATCAATATGAA<br>CTT/GJCGTATTG<br>GATTAGTGGTG<br>AGAAGA   | T | G | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD45179<br>RIBONUCLEOPROTEIN - HOMO<br>SAPIENS (HUMAN), 346 aa.                             | 4.50E-152 | 14 |
| 563 | cg43951092 | 1616 | TATCAATATGAA<br>CTCGTATTGGAT<br>TTT/GJAGTGGTG<br>AGAAGAAATTAG<br>CAATGT  | T | G | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD45179<br>RIBONUCLEOPROTEIN - HOMO<br>SAPIENS (HUMAN), 346 aa.                             | 4.50E-152 | 14 |
| 564 | cg43951092 | 1640 | TTAGTGGTGAG<br>AAGAAATTAGCA<br>AT[G/A]TCATTTT<br>CAGTTGCACGA<br>AAAGGCA  | G | A | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD45179<br>RIBONUCLEOPROTEIN - HOMO<br>SAPIENS (HUMAN), 346 aa.                             | 4.50E-152 | 14 |
| 565 | cg43990820 | 1135 | CATCAGTTTCCA<br>CTTCGACACATC<br>G[G/A]TAGTCCT<br>CACAGCCACGG<br>CCATCCA  | G | A | Tyr | Tyr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q15024 MRNA<br>(HA0800) FOR ORF - HOMO<br>SAPIENS (HUMAN), 290 aa<br>(fragment). | 3.30E-150 | 3  |
| 566 | cg43990820 | 724  | TCGACCCCTCTT<br>CATCCTCCAAAA<br>CTT/CJCGAACCC<br>TTGGTATCCTTG<br>TATTGA  | T | C | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q15024 MRNA<br>(HA0800) FOR ORF - HOMO<br>SAPIENS (HUMAN), 290 aa<br>(fragment). | 3.30E-150 | 3  |





|     |            |     |   |   |     |                   |                  |   |           |  |
|-----|------------|-----|---|---|-----|-------------------|------------------|---|-----------|--|
| 572 | cg29351416 | 546 | AGTTCCAAAGTAG<br>ACAAACAGTAATC<br>G[C/T]CTGTTACT<br>GCAGCAGGTCT<br>CATTAC | T | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q03626 ALPHA-1-<br>INHIBITOR III PRECURSOR,<br>ISOFORM 2 (RAT PLASMA<br>PROTEINASE INHIBITOR ALPHA-1-<br>INHIBITOR III GROUP 3 VARIANT<br>36A) (ALPHA-1 PROTEINASE<br>INHIBITOR 3, EXONS 1-4) - RATTUS<br>NORVEGICUS (RAT), 1487 aa. | 3.20E-127 |  |
| 573 | cg29351416 | 645 | TGTATGCTCAGA<br>CCACGCTGAGA<br>TA[C/T]AACATGC<br>CCTTGGAGAAG<br>CAGCAGC   | T | Tyr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q03626 ALPHA-1-<br>INHIBITOR III PRECURSOR,<br>ISOFORM 2 (RAT PLASMA<br>PROTEINASE INHIBITOR ALPHA-1-<br>INHIBITOR III GROUP 3 VARIANT<br>36A) (ALPHA-1 PROTEINASE<br>INHIBITOR 3, EXONS 1-4) - RATTUS<br>NORVEGICUS (RAT), 1487 aa. | 3.20E-127 |  |
| 574 | cg29351416 | 648 | ATGCTCAGACC<br>ACGCTGAGATA<br>CAA[C/T]ATGCC<br>CTTGGAGAAGC<br>AGCAGCCTG   | T | Asn | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q03626 ALPHA-1-<br>INHIBITOR III PRECURSOR,<br>ISOFORM 2 (RAT PLASMA<br>PROTEINASE INHIBITOR ALPHA-1-<br>INHIBITOR III GROUP 3 VARIANT<br>36A) (ALPHA-1 PROTEINASE<br>INHIBITOR 3, EXONS 1-4) - RATTUS<br>NORVEGICUS (RAT), 1487 aa. | 3.20E-127 |  |
| 575 | cg43950273 | 530 | GGTCTTCAATAA<br>AGTAGTTATGGC<br>A[C/A]GTCCTGA<br>TCCACATAGATA<br>GCTGAA   | A | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:CAB45700<br>HYPOTHETICAL 32.5 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 287 aa<br>(fragment).   | 2.40E-123 |  |



|     |            |     |   |   |   |     |     |                   |                  |  |           |  |
|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|--|-----------|--|
| 580 | cg44930828 | 603 | CTCGAGGTGAG<br>AAACCCCAATCCT<br>TT[G/A]AGGCAA<br>AAGAACGCCAA<br>GGTGAACC  | G | A | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:Q29459<br>PLATELET-ACTIVATING FACTOR<br>ACETYLDHIDROLASE IB BETA<br>SUBUNIT (EC 3.1.1.47) (PAF<br>ACETYLDHIDROLASE 30 KD<br>SUBUNIT) (PAF-AH 30 KD<br>SUBUNIT) (PAF-AH BETA SUBUNIT)<br>- Homo sapiens (Human), and Bos<br>taurus (Bovine), 229 aa. | 3.10E-122 |  |
| 581 | cg44930828 | 615 | AACCCCAATCCTT<br>TGAGGCAAAAG<br>AA[C/T]GCCAAG<br>GTGAACCAACT<br>CCTCAAGG  | C | T | Asn | Asn | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:Q29459<br>PLATELET-ACTIVATING FACTOR<br>ACETYLDHIDROLASE IB BETA<br>SUBUNIT (EC 3.1.1.47) (PAF<br>ACETYLDHIDROLASE 30 KD<br>SUBUNIT) (PAF-AH 30 KD<br>SUBUNIT) (PAF-AH BETA SUBUNIT)<br>- Homo sapiens (Human), and Bos<br>taurus (Bovine), 229 aa. | 3.10E-122 |  |
| 582 | cg44930828 | 630 | GGCAAAAAGAAC<br>GCCAAGGTGAA<br>CCA[A/G]CTCCT<br>CAAGGTTTCGCT<br>GCCGAAAGC | A | G | Gln | Gln | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:Q29459<br>PLATELET-ACTIVATING FACTOR<br>ACETYLDHIDROLASE IB BETA<br>SUBUNIT (EC 3.1.1.47) (PAF<br>ACETYLDHIDROLASE 30 KD<br>SUBUNIT) (PAF-AH 30 KD<br>SUBUNIT) (PAF-AH BETA SUBUNIT)<br>- Homo sapiens (Human), and Bos<br>taurus (Bovine), 229 aa. | 3.10E-122 |  |
| 583 | cg44930828 | 645 | AGGTGAACCAA<br>CTCCTCAAGGTT<br>TC[G/C]CTGCCG<br>AAGCTTGCCAA<br>CGTGCAGC   | G | C | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:Q29459<br>PLATELET-ACTIVATING FACTOR<br>ACETYLDHIDROLASE IB BETA<br>SUBUNIT (EC 3.1.1.47) (PAF<br>ACETYLDHIDROLASE 30 KD<br>SUBUNIT) (PAF-AH 30 KD<br>SUBUNIT) (PAF-AH BETA SUBUNIT)<br>- Homo sapiens (Human), and Bos<br>taurus (Bovine), 229 aa. | 3.10E-122 |  |

|     |            |     |  |   |   |     |     |                   |                  |  |           |  |
|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|--|-----------|--|
| 584 | cg44930828 | 663 | AGGTTTCGCTG<br>CCGAAGCTTGC<br>CAA[C/T]GTGCA<br>GCTCCTGGATA<br>CCGACGGGG    | C | T | Asn | Asn | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:Q29459<br>PLATELET-ACTIVATING FACTOR<br>ACETYLHYDROLASE IB BETA<br>SUBUNIT (EC 3.1.1.47) (PAF<br>ACETYLHYDROLASE 30 KD<br>SUBUNIT) (PAF-AH 30 KD<br>SUBUNIT) (PAF-AH BETA SUBUNIT)<br>- Homo sapiens (Human), and Bos<br>taurus (Bovine), 229 aa. | 3.10E-122 |  |
| 585 | cg44930828 | 690 | TGCAGTCCTG<br>GATACCGACGG<br>GGG[T/C]TTGT<br>GCACTCGGACG<br>GTGCCATCT      | T | C | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:Q29459<br>PLATELET-ACTIVATING FACTOR<br>ACETYLHYDROLASE IB BETA<br>SUBUNIT (EC 3.1.1.47) (PAF<br>ACETYLHYDROLASE 30 KD<br>SUBUNIT) (PAF-AH 30 KD<br>SUBUNIT) (PAF-AH BETA SUBUNIT)<br>- Homo sapiens (Human), and Bos<br>taurus (Bovine), 229 aa. | 3.10E-122 |  |
| 586 | cg44930828 | 693 | AGTCCTCGGAT<br>ACCGACGGGG<br>TTT[T/C]GTGCAC<br>TCGGACGGTGC<br>CATCTCCT     | T | C | Phe | Phe | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:Q29459<br>PLATELET-ACTIVATING FACTOR<br>ACETYLHYDROLASE IB BETA<br>SUBUNIT (EC 3.1.1.47) (PAF<br>ACETYLHYDROLASE 30 KD<br>SUBUNIT) (PAF-AH 30 KD<br>SUBUNIT) (PAF-AH BETA SUBUNIT)<br>- Homo sapiens (Human), and Bos<br>taurus (Bovine), 229 aa. | 3.10E-122 |  |
| 587 | cg43975478 | 691 | AAACCCCTGAG<br>AAAAGATACAAT<br>GT[C/T]CTGGGA<br>GCTGAGACTGT<br>GCTCAATC    | C | T | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q63555 SP120 -<br>RATTUS NORVEGICUS (RAT), 798<br>aa.   | 4.10E-119 |  |
| 588 | cg42530218 | 601 | GCATGCCCCAGT<br>AATAAAGATGAA<br>GAT[C/G]GGGCTA<br>GTGGTTTGTAGTT<br>TTCAACA | T | C | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:P70582<br>NUCLEOPORIN P54 - RATTUS<br>NORVEGICUS (RAT), 510 aa.   | 2.00E-118 |  |



|     |            |     |  |   |   |     |     |                   |                  |  |           |    |
|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|--|-----------|----|
| 596 | cg43986282 | 794 | GCACCTCTTCTG<br>CGTGGTACACG<br>GT[C/T]CTCCCA<br>CAGGCCCCACA<br>CTTGTTTC  | C | T | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:P97314 DOUBLE<br>LIM PROTEIN-1 - MUS MUSCULUS<br>(MOUSE), 193 aa. | 2.90E-110 | 12 |
| 597 | cg43986282 | 800 | CTTCTGCGTGG<br>TACACGGTCCT<br>CCC[A/G]CAGGC<br>CCCACACTTGT<br>TCCACCTC   | A | G | Cys | Cys | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:P97314 DOUBLE<br>LIM PROTEIN-1 - MUS MUSCULUS<br>(MOUSE), 193 aa. | 2.90E-110 | 12 |
| 598 | cg43986282 | 809 | GGTACACGGTC<br>CTCCACAGGC<br>CCC[A/G]CACTT<br>GTTCCACCTCC<br>CCAGACAG    | A | G | Cys | Cys | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:P97314 DOUBLE<br>LIM PROTEIN-1 - MUS MUSCULUS<br>(MOUSE), 193 aa. | 2.90E-110 | 12 |
| 599 | cg43986282 | 815 | CGGTCCTCCCA<br>CAGGCCCCACA<br>CTT[G/A]TTTCCA<br>CCTCCCCAGAC<br>AGGCATTTC | G | A | Asn | Asn | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:P97314 DOUBLE<br>LIM PROTEIN-1 - MUS MUSCULUS<br>(MOUSE), 193 aa. | 2.90E-110 | 12 |
| 600 | cg42723058 | 651 | GTCCCTTACCA<br>CCACCGGTCAC<br>AGA[T/C]GTGAG<br>CCTTGAGTTGCA<br>GCAGCTGC  | T | C | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:BAA82158 HCR<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 756 aa.       | 1.70E-107 |    |
| 601 | cg42723058 | 673 | AGATGTGAGCC<br>TTGAGTTGCAG<br>CAG[C/T]TGC GG<br>GAAGAACGGAA<br>CCGCCTGGA | C | T | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:BAA82158 HCR<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 756 aa.       | 1.70E-107 |    |





|     |            |     |   |   |   |     |     |                   |                  |   |           |    |
|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|---|-----------|----|
| 609 | cg44911139 | 722 | GCAAGGTTTCG<br>GATGTACGTATC<br>ATC/TTCAGATC<br>GGAACACACGT<br>CGTCTA    | C | T | Ile | Ile | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q1499 SPLICING<br>FACTOR - HOMO SAPIENS<br>(HUMAN), 530 aa.    | 7.90E-101 | 14 |
| 610 | cg42539705 | 165 | AAAGGAACTAT<br>TTCCAGATGAG<br>GC[G/A]GGGTGT<br>CTGGAGGGGC<br>TGTGGGTG   | G | A | Pro | Pro | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O75229 R31449_3 - HOMO<br>SAPIENS (HUMAN), 813 aa<br>(fragment). | 1.20E-100 |    |
| 611 | cg42028329 | 115 | CCAAGGAGAAC<br>CCGTGCAGAA<br>ATT[C/T]CAGGC<br>CAACATCTTCAA<br>CAAGAGCA  | C | T | Phe | Phe | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P97434 P116RIP - MUS<br>MUSCULUS (MOUSE), 1024 aa.               | 2.40E-99  |    |
| 612 | cg42028329 | 277 | ACTTTGACAACC<br>CAGTACACCGG<br>TC[T/A]CGGAA<br>TGGCAGCGACG<br>GTTCTTCA  | T | A | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P97434 P116RIP - MUS<br>MUSCULUS (MOUSE), 1024 aa.               | 2.40E-99  |    |
| 613 | cg42028329 | 295 | ACCGGTCTCGG<br>AAATGGCAGCG<br>ACG[G/A]TTCTT<br>CATCCTTTACGA<br>GCACGGCC | G | A | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P97434 P116RIP - MUS<br>MUSCULUS (MOUSE), 1024 aa.               | 2.40E-99  |    |
| 614 | cg42028329 | 310 | GGCAGCGACGG<br>TTCCTCATCCTT<br>TA[C/T]GAGCAC<br>GGCCTCTTGGC<br>CTACGCC  | C | T | Tyr | Tyr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P97434 P116RIP - MUS<br>MUSCULUS (MOUSE), 1024 aa.               | 2.40E-99  |    |
| 615 | cg42028329 | 316 | GACGGTCTTCA<br>TCCTTTACGAGC<br>A[C/T]GGCCTCT<br>TGCCTACGCC<br>CTGGATG   | C | T | His | His | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P97434 P116RIP - MUS<br>MUSCULUS (MOUSE), 1024 aa.               | 2.40E-99  |    |

|     |            |     |   |   |   |     |     |                   |                  |  |          |  |
|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|--|----------|--|
| 616 | cg42028329 | 328 | TCCTTTACGAGC<br>ACGGCCTCTTG<br>CGC/AJTACGCC<br>CTGGATGAGAT<br>GCCACAGA  | C | A | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P97434 P116RIP - MUS<br>MUSCULUS (MOUSE), 1024 aa.                          | 2.40E-99 |  |
| 617 | cg42028329 | 352 | GCTACGCCCTG<br>GATGAGATGCC<br>CAC/GCJACCCT<br>TCCTCAGGGCA<br>CCATCAACA  | G | C | Thr | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P97434 P116RIP - MUS<br>MUSCULUS (MOUSE), 1024 aa.                          | 2.40E-99 |  |
| 618 | cg42392719 | 540 | TCGCGAGAACG<br>GCCTCAGTGCC<br>AAG[G/T]CCCTT<br>ACCCCTGCAGC<br>TGGGCTCTG | G | T | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB43370<br>HYPOTHETICAL 23.3 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 206 aa. | 6.40E-99 |  |
| 619 | cg42392719 | 606 | TCTCCCCCAAG<br>GTGGGGTCTTC<br>TAG[A/G]TCTGT<br>GAGGAAGAGGT<br>TCACATCTC | A | G | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB43370<br>HYPOTHETICAL 23.3 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 206 aa. | 6.40E-99 |  |
| 620 | cg42392719 | 627 | CTAGATCTGTGA<br>GGAAGAGGTTT<br>AC[A/G]TCTCCC<br>ACCATGCAGCT<br>CTCTTCAG | A | G | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB43370<br>HYPOTHETICAL 23.3 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 206 aa. | 6.40E-99 |  |
| 621 | cg39512856 | 597 | ACGCGTCGCCG<br>GAAGCCACGTC<br>ATA[G/A]ACGGT<br>TTTACCCCGATG<br>GTCTTCAA | G | A | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.   | 1.20E-98 |  |
| 622 | cg39512856 | 615 | CGTCATAGACG<br>GTTTACCCCGA<br>TG[G/A]TCTTCAA<br>CGAGATGCCAC<br>GATGCCT  | G | A | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.   | 1.20E-98 |  |

|     |            |     |  |   |   |     |     |                   |                  |   |          |    |
|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|---|----------|----|
| 623 | cg39512856 | 663 | CCTCATCACTGT<br>TGAAACAGCC<br>AC/A/GAAGCCA<br>GCCGGAATATC<br>TGGCGGTG  | A | G | Phe | Phe | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.  | 1.20E-98 |    |
| 624 | cg39512856 | 690 | AGCCAGCCGGA<br>ATATCTGGCGG<br>TGC/A/GATATC<br>GGTACTGTTTGC<br>AGCAGAC  | A | G | Ile | Ile | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.  | 1.20E-98 |    |
| 625 | cg39512856 | 708 | GCGGTGCAATA<br>TCGGTACTGTTT<br>GC/A/TGGCAGA<br>CCGGTATGAGG<br>CGGAATAT | A | T | Pro | Pro | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.  | 1.20E-98 |    |
| 626 | cg39512856 | 717 | TATCGGTACTGT<br>TTGCAGGCAGA<br>CC/G/TGTATGA<br>GGCGGAATATA<br>TGCGTAC  | G | T | Thr | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.  | 1.20E-98 |    |
| 627 | cg37445474 | 599 | CCCTGCAAGCT<br>CTGTATGGAAC<br>GATC/TCCCCA<br>GATCTTTGGGA<br>AGGAGAAT   | C | T | Ile | Ile | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q63615 VACUOLAR PROTEIN<br>SORTING HOMOLOG R-VPS33A -<br>RATTUS NORVEGICUS (RAT), 597<br>aa.                                   | 2.80E-96 |    |
| 628 | cg30791729 | 294 | CAGATCCAGTG<br>GCCTTCCCCCA<br>GCTG/TJGTCA<br>ACTGTGTCCAG<br>GCTGTGGCT  | G | T | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:P12346 SEROTRANSFERRIN<br>PRECURSOR (SIDEROPHILIN)<br>(BETA-1-METAL BINDING<br>GLOBULIN) - Rattus norvegicus<br>(Rat), 698 aa. | 3.20E-95 |    |
| 629 | cg42522690 | 454 | GTGAACAGTGT<br>AAATCAGTTTT<br>CA/T/CJTGGGAC<br>ATGAAATCCAAG<br>GATAAGG | T | C | His | His | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O35884 NEBULIN-RELATED<br>ANCHORING PROTEIN (N-RAP) -<br>MUS MUSCULUS (MOUSE), 1175<br>aa.                                     | 3.30E-94 | 10 |

|     |            |     |   |   |   |     |     |                   |                  |   |          |    |
|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|---|----------|----|
| 630 | cg42522690 | 625 | CTCGAAAGTCTC<br>TTGGTGAGGAA<br>TA[T/C]ACAGAA<br>GACTATGAGCA<br>ACCCAGGG | T | C | Tyr | Tyr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O35884 NEBULIN-RELATED<br>ANCHORING PROTEIN (N-RAP) -<br>MUS MUSCULUS (MOUSE), 1175<br>aa. | 3.30E-94 | 10 |
| 631 | cg43982164 | 561 | AGGTCTACGTG<br>TTGAAGCGTCCT<br>CA[T/C]GTGGAT<br>GAGTTCCTGCA<br>GCGAATGG | T | C | His | His | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O15194 HYA22 - HOMO<br>SAPIENS (HUMAN), 340 aa.  | 1.00E-90 |    |
| 632 | cg43980889 | 755 | AAGACCAATTAC<br>AAGTAGAAAATG<br>A[T/C]GCTTACC<br>CTGGTACCGAT<br>AGAACAG | T | C | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O00581 HYPOTHETICAL 20.5<br>KD PROTEIN - HOMO SAPIENS<br>(HUMAN), 176 aa.                  | 4.50E-89 |    |
| 633 | cg43980889 | 770 | TAGAAAATGATG<br>CTTACCCTGGTA<br>C[C/T]GATAGAA<br>CAGAAAATGTTA<br>AATATA | C | T | Thr | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O00581 HYPOTHETICAL 20.5<br>KD PROTEIN - HOMO SAPIENS<br>(HUMAN), 176 aa.                  | 4.50E-89 |    |
| 634 | cg43980889 | 776 | ATGATGCTTACC<br>CTGGTACCGAT<br>AG[A/G]ACAGAA<br>AATGTTAAATAT<br>AGACAAG | A | G | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O00581 HYPOTHETICAL 20.5<br>KD PROTEIN - HOMO SAPIENS<br>(HUMAN), 176 aa.                  | 4.50E-89 |    |
| 635 | cg43980889 | 791 | GTACCGATAGA<br>ACAGAAAATGTT<br>AA[A/G]TATAGA<br>CAAGTGGACCA<br>TTTTGCCT | A | G | Lys | Lys | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O00581 HYPOTHETICAL 20.5<br>KD PROTEIN - HOMO SAPIENS<br>(HUMAN), 176 aa.                  | 4.50E-89 |    |
| 636 | cg43955651 | 449 | CTTCCACCACG<br>CCTGTGTTCTG<br>GGC[G/A]CTGAC<br>AAAGGCCACCT<br>TGTTGGTGT | G | A | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD27745 CGI-<br>36 PROTEIN - HOMO SAPIENS<br>(HUMAN), 165 aa.                             | 1.10E-87 | 2  |

|     |            |      |  |   |   |     |     |                   |                  |  |          |   |
|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|--|----------|---|
| 637 | cg4395651  | 476  | TGACAAAGGCC<br>ACCTTGTTGGTG<br>TC[G/A]GGCTTG<br>AGCGGAATGAA<br>GCCACACT  | G | A | Pro | Pro | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD2745 CGI-<br>36 PROTEIN - HOMO SAPIENS<br>(HUMAN), 165 aa.   | 1.10E-87 | 2 |
| 638 | cg42353267 | 1516 | GGCCTTCGATC<br>CAGTCCATGAG<br>CAA[T/C]GCCAT<br>ATAGCGCGGCG<br>CAGAGAGCT  | T | C | Ala | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O75249 R26660_1, PARTIAL<br>CDS - HOMO SAPIENS (HUMAN),<br>291 aa (fragment).   | 2.60E-86 |   |
| 639 | cg37027086 | 258  | GGGTTCTTCAAC<br>TGGGACAGGAG<br>GC[T/C]TCTACC<br>CACCAGGCCCA<br>AAACGAGG  | T | C | Ala | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA76824<br>KIAA0980 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1406 aa<br>(fragment).  | 1.20E-83 |   |
| 640 | cg42688841 | 449  | TCAACATAAGGT<br>AGAAATTCATTA<br>A[C/T]CTCAAGA<br>AGCGAGCGTCA<br>TAGTATA  | C | T | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:Q02380 NADH-UBIQUINONE<br>OXIDOREDUCTASE SGD<br>SUBUNIT PRECURSOR (EC 1.6.5.3)<br>(EC 1.6.99.3) (COMPLEX I-SGDH)<br>(CI-SGDH) - Bos taurus (Bovine), 189<br>aa. | 1.90E-83 |   |
| 641 | cg42688841 | 454  | ATAAGGTAGAAT<br>TTCATTAACCTC<br>A[A/G]GAAGCGA<br>GCGTCATAGTAT<br>AAAAGAA | A | G | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:Q02380 NADH-UBIQUINONE<br>OXIDOREDUCTASE SGD<br>SUBUNIT PRECURSOR (EC 1.6.5.3)<br>(EC 1.6.99.3) (COMPLEX I-SGDH)<br>(CI-SGDH) - Bos taurus (Bovine), 189<br>aa. | 1.90E-83 |   |
| 642 | cg42688841 | 461  | AGAAATTCATTA<br>ACCTCAAGAAAG<br>CG[A/G]GCGTCA<br>TAGTATAAGAA<br>GGCTTGA  | A | G | Ala | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:Q02380 NADH-UBIQUINONE<br>OXIDOREDUCTASE SGD<br>SUBUNIT PRECURSOR (EC 1.6.5.3)<br>(EC 1.6.99.3) (COMPLEX I-SGDH)<br>(CI-SGDH) - Bos taurus (Bovine), 189<br>aa. | 1.90E-83 |   |

|     |            |      |  |   |   |     |                   |                  |  |          |   |
|-----|------------|------|--|---|---|-----|-------------------|------------------|--|----------|---|
| 643 | cg4268841  | 476  | TCAAGAAGCGA<br>GCGTCATAGTAT<br>AA[A/G]GAAGGC<br>TTGACGACAAAC<br>AGTCTCT  | A | G | Ser | Silent-<br>Coding | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:Q02380 NADH-UBIQUINONE<br>OXIDOREDUCTASE SGD<br>SUBUNIT PRECURSOR (EC 1.6.5.3)<br>(EC 1.6.99.3) (COMPLEX I-SGDH)<br>(CI-SGDH) - Bos taurus (Bovine), 189<br>aa. | 1.90E-83 |   |
| 644 | cg43982291 | 1590 | CACTGTGACCAT<br>TTTGTACAGCAA<br>G[A/C]JAGCAGCG<br>GTATATTCCCAT<br>CCAAAT | A | C | Leu | Silent-<br>Coding | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q28282 C3VS PROTEIN -<br>CANIS FAMILIARIS (DOG), 659 aa.  | 3.20E-79 |   |
| 645 | cg43982291 | 1716 | GTAAAGCTGTTT<br>TCCCAGAGCTG<br>TC[G/A]JACACTTT<br>CGGCTGGGCAT<br>TTAGACT | G | A | Val | Silent-<br>Coding | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q28282 C3VS PROTEIN -<br>CANIS FAMILIARIS (DOG), 659 aa.  | 3.20E-79 |   |
| 646 | cg44003673 | 320  | CATGCTTGGTG<br>CCTGGTGCCAG<br>GTG[A/G]GTGAT<br>GACGACCTCCA<br>CGGCCTGCA  | A | G | Thr | Silent-<br>Coding | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD25021<br>CALCIUM-REGULATED HEAT<br>STABLE PROTEIN CRHSP-24 -<br>HOMO SAPIENS (HUMAN), 147 aa.  | 1.60E-77 |   |
| 647 | cg44003673 | 449  | CATCAGAGATGT<br>GCAGGAAGATG<br>TC[G/A]GGGCCG<br>CCATCAGCTGG<br>GGTAATGA  | G | A | Pro | Silent-<br>Coding | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD25021<br>CALCIUM-REGULATED HEAT<br>STABLE PROTEIN CRHSP-24 -<br>HOMO SAPIENS (HUMAN), 147 aa.  | 1.60E-77 |   |
| 648 | cg44003673 | 470  | TGTCGGGGCCG<br>CCATCAGCTGG<br>GGT[A/G]ATGAA<br>GCCATGGCCCT<br>TGGACCGGC  | A | G | Ile | Silent-<br>Coding | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD25021<br>CALCIUM-REGULATED HEAT<br>STABLE PROTEIN CRHSP-24 -<br>HOMO SAPIENS (HUMAN), 147 aa.  | 1.60E-77 |   |
| 649 | cg44936941 | 1207 | CGCGCACCTCG<br>TCGCCGATCTG<br>CTGT[C]CCGGT<br>CTCCTTGCCGA<br>GGAAGTCGT   | T | C | Gly | Silent-<br>Coding | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q62630 SM-20 - RATTUS<br>NORVEGICUS (RAT), 355 aa.  | 7.00E-77 | 1 |

|     |            |     |  |   |   |     |     |                   |                  |  |          |  |
|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|--|----------|--|
| 650 | cg39523553 | 704 | GGTCTGCCCGA<br>TCCGGGATGGC<br>TGC[A]GGTGG<br>GTGATCGACGG<br>TAGGCCGGA    | C | A | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa. | 7.20E-75 |  |
| 651 | cg39523553 | 721 | ATGGCTGCCCG<br>TGGGTGATCGA<br>CGG[T/C]AGGCC<br>GGACAATGCC<br>CGGCCCGTC   | T | C | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa. | 7.2E-75  |  |
| 652 | cg39523553 | 772 | GAGGACAGCCA<br>TGGAAAGGGCAC<br>GGA[T/C]CGCCA<br>GTGCCCGCGCG<br>TGATTATGG | T | C | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa. | 7.2E-75  |  |
| 653 | cg39523553 | 823 | ACGTGGTGCGC<br>AACAGCCCTCA<br>CGG[A/G]GTGAA<br>GGTCCAGATGG<br>CTCTTTCCG  | A | G | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa. | 7.2E-75  |  |
| 654 | cg39523553 | 874 | CCTGGCCCGAG<br>CTCGATCAGGC<br>ATC[A/G]AGGTG<br>CCTGGAATCCTT<br>ACTCGATG  | A | G | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa. | 7.2E-75  |  |
| 655 | cg39523553 | 886 | TCGATCAGGCA<br>TCAAGGTGCCT<br>GGA[A/G]TCCTT<br>ACTCGATGACG<br>GTTTAGTGC  | A | G | Glu | Glu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa. | 7.2E-75  |  |

|     |            |     |  |   |   |     |     |                   |                  |  |          |    |
|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|--|----------|----|
| 656 | cg36728314 | 399 | GCTGCTGCTTCT<br>TCCTTGTTGGAA<br>C[G/A]ATCTTCT<br>GGGCAACGTCC<br>TGGAAGA  | G | A | Ile | Ile | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA83051<br>KIAA1099 PROTEIN - HOMO<br>SAPIENS (HUMAN), 804 aa.                       | 1.3E-73  |    |
| 657 | cg41677120 | 375 | TTCAGTGCACAA<br>ATGAGATGAATG<br>T[G/T]AACATCC<br>CACAGTTGGCA<br>GACAGTT  | G | T | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q13492 CALM (TYPE I CALM<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 652 aa.               | 1.10E-71 | 11 |
| 658 | cg44126579 | 655 | AGGAGTATTCAT<br>CATCCCCAATG<br>CC[G/A]TAGCCT<br>TCATGATTGAGG<br>AATTGTC  | G | A | Tyr | Tyr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P90839 F16A11.1 -<br>CAENORHABDITIS ELEGANS, 673<br>aa.                               | 1.10E-71 | 16 |
| 659 | cg44126579 | 712 | GAGTGGCCCAG<br>CCAAATCTGCATG<br>AC[G/A]CCAGAA<br>GTGACCACTGTT<br>ACTTCAT | G | A | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P90839 F16A11.1 -<br>CAENORHABDITIS ELEGANS, 673<br>aa.                               | 1.10E-71 | 16 |
| 660 | cg38925480 | 73  | AGAAATCTCACCA<br>GCCTTGTGGTG<br>CT[G/A]CATTG<br>CATAACAACCG<br>CATCCAGC  | G | A | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O75473 ORPHAN G PROTEIN-<br>COUPLED RECEPTOR HG38 -<br>HOMO SAPIENS (HUMAN), 907 aa.  | 4.90E-69 |    |
| 661 | cg43323149 | 544 | GCACACGCGGA<br>AGCCCTACAGA<br>CG[G/A]CTCAG<br>CGTCATGCAAG<br>GGCCCTACA   | A | G | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P50636 GAMETOGENESIS<br>EXPRESSED PROTEIN GEG-154 -<br>Mus musculus (Mouse), 429 aa. | 1.00E-68 | 1  |
| 662 | cg43323149 | 559 | CTACAGACGGA<br>CTCAGCGTCAT<br>GCAI[A/G]GGGCC<br>CTACAGCGGAA<br>CAGCCAGCT | A | G | Gln | Gln | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P50636 GAMETOGENESIS<br>EXPRESSED PROTEIN GEG-154 -<br>Mus musculus (Mouse), 429 aa. | 1.00E-68 | 1  |



|     |            |     |  |   |   |     |     |                   |                  |  |          |   |
|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|--|----------|---|
| 663 | cg43323149 | 664 | GAAATACAGC<br>CGGTTAGAGTT<br>CA[A/G]GCCGAT<br>GTCCAAAAGGA<br>AATTTTCC    | A | G | Gln | Gln | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P50636 GAMETOGENESIS<br>EXPRESSED PROTEIN GEG-154 -<br>Mus musculus (Mouse), 429 aa. | 1.00E-68 | 1 |
| 664 | cg34243633 | 263 | CCACCACAGAG<br>ATAATGCAGGC<br>CAG[G/C]CAGGA<br>GATTGCACTGG<br>ATGTCACCA  | G | C | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O88552 CLAUDIN-2 - MUS<br>MUSCULUS (MOUSE), 230 aa.                                   | 1.3E-68  |   |
| 665 | cg34243633 | 431 | CAACTGCTGTCA<br>CAATGCTGGCA<br>CC[G/A]ACATAA<br>GAAC TTGTTTC<br>CAGCTGG  | G | A | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O88552 CLAUDIN-2 - MUS<br>MUSCULUS (MOUSE), 230 aa.                                   | 1.3E-68  |   |
| 666 | cg34243633 | 482 | GGAGCAGCATG<br>GCAACCAGTGT<br>GCC[C/T]AAAAG<br>CCCCAGAAGGC<br>CTAGGATGT  | C | T | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O88552 CLAUDIN-2 - MUS<br>MUSCULUS (MOUSE), 230 aa.                                   | 1.3E-68  |   |
| 667 | cg43942922 | 231 | AGCCCACATCT<br>CAGGCCACTAG<br>GGG[C/A]AGAAC<br>AAATAGGTCCTC<br>TGTC AAGA | C | A | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14676 KIAA0170 PROTEIN -<br>HOMO SAPIENS (HUMAN), 2089 aa.                           | 2.3E-68  |   |
| 668 | cg43942922 | 291 | CAGTTGTCCCC<br>ACAGCCCCTGA<br>GCT[C/T]CAGCC<br>TTCCACCTCCAC<br>AGACCAGC  | C | T | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14676 KIAA0170 PROTEIN -<br>HOMO SAPIENS (HUMAN), 2089 aa.                           | 2.3E-68  |   |



|     |            |     |   |   |   |     |     |                   |                  |   |          |  |
|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|---|----------|--|
| 676 | cg39516123 | 563 | TCAGCTCCTCTC<br>CGGAAAGCCAG<br>GC[C]CGAGCT<br>CAGTTCAGTGT<br>GGCTGGCG   | C | T | Ala | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q04205 TENSIN - Gallus gallus<br>(Chicken), 1744 aa.  | 5.1E-62  |  |
| 677 | cg39516123 | 620 | CGGTGCCTGGG<br>AGCCCTCAGGC<br>GCG[C]T]CACAG<br>AACAGTGGGCA<br>CCAACAGTC | C | T | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q04205 TENSIN - Gallus gallus<br>(Chicken), 1744 aa.  | 5.1E-62  |  |
| 678 | cg42731307 | 435 | GGAATGAGCC<br>AAAGTTCGCATG<br>AA[T]C]CCACGG<br>AAGTTTACCTGG<br>TCCTCTC  | T | C | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q99653 CALCIUM-BINDING<br>PROTEIN P22 (CALCIUM-BINDING<br>PROTEIN CHP) - Homo sapiens<br>(Human), 194 aa. | 2.6E-61  |  |
| 679 | cg44128084 | 440 | CCGGACAAAC<br>CGTTGGAGTTCT<br>TT[T]C]GCCGTC<br>AACGAGTTGTCT<br>CTGGAAA  | T | C | Phe | Phe | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O33196 HYPOTHETICAL 32.9<br>KD PROTEIN - MYCOBACTERIUM<br>TUBERCULOSIS, 307 aa.                            | 1.70E-59 |  |
| 680 | cg44128084 | 665 | TGAGCGCTCAC<br>GCTCTCTTTGCT<br>CG[A]G]CCGCTG<br>GTCATGAGCCC<br>AGCTGCTC | A | G | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O33196 HYPOTHETICAL 32.9<br>KD PROTEIN - MYCOBACTERIUM<br>TUBERCULOSIS, 307 aa.                            | 1.70E-59 |  |
| 681 | cg44128084 | 680 | TCTTTGCTCGAC<br>CGCTGGTCATG<br>AG[C]T]CCAGCT<br>GCTCGAGTGGA<br>CCTTGACA | C | T | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O33196 HYPOTHETICAL 32.9<br>KD PROTEIN - MYCOBACTERIUM<br>TUBERCULOSIS, 307 aa.                            | 1.70E-59 |  |
| 682 | cg44128084 | 695 | TGGTCATGAGC<br>CCAGCTGCTCG<br>AGT[G/A]GACCT<br>TGACATCCAGC<br>CAGACGGTT | G | A | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O33196 HYPOTHETICAL 32.9<br>KD PROTEIN - MYCOBACTERIUM<br>TUBERCULOSIS, 307 aa.                            | 1.70E-59 |  |



|     |            |     |  |   |   |     |     |                   |                  |   |          |  |
|-----|------------|-----|--|---|---|-----|-----|-------------------|------------------|---|----------|--|
| 690 | cg43153425 | 128 | GTGACCGAGAG<br>ATCAGCATGTCT<br>GT[C/T]GGTCTG<br>GGAAGGTCACA<br>GTTAGACT  | C | T | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA83061<br>KIAA1109 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1957 aa<br>(fragment). | 2.40E-57 |  |
| 691 | cg43153425 | 140 | TCAGCATGTCTG<br>TCGGTCTGGGA<br>AG[G/A]TCACAG<br>TTAGACTCCAAA<br>GGAGGAG  | G | A | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA83061<br>KIAA1109 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1957 aa<br>(fragment). | 2.40E-57 |  |
| 692 | cg43153425 | 146 | TGTCTGTCTGGT<br>CTGGGAAGGTC<br>ACA[G/A]TTAGA<br>CTCCAAAGGAG<br>GAGTAGTTG | G | A | Gln | Gln | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA83061<br>KIAA1109 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1957 aa<br>(fragment). | 2.40E-57 |  |
| 693 | cg43153425 | 152 | TCGGTCTGGGA<br>AGGTCACAGTTA<br>GA[C/T]TCCAAA<br>GGAGGAGTAGT<br>TGGTGGGA  | C | T | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA83061<br>KIAA1109 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1957 aa<br>(fragment). | 2.40E-57 |  |
| 694 | cg43153425 | 155 | GTCTGGGAAGG<br>TCACAGTTAGAC<br>TC[C/T]AAAGGA<br>GGAGTAGTTGG<br>TGGGACCA  | C | T | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA83061<br>KIAA1109 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1957 aa<br>(fragment). | 2.40E-57 |  |
| 695 | cg43153425 | 251 | CAAATCAGCAAC<br>CAAACCACAAAA<br>T[A/T]CAAAATTAC<br>TATGGGTTCTAC<br>TGAAT | A | T | Ile | Ile | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA83061<br>KIAA1109 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1957 aa<br>(fragment). | 2.40E-57 |  |
| 696 | cg43153425 | 287 | TGGGTTCTACTG<br>AATCTCGGGTT<br>GA[C/T]TACATG<br>GGCTCAAGCAT<br>CCTCATGG  | C | T | Asp | Asp | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA83061<br>KIAA1109 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1957 aa<br>(fragment). | 2.40E-57 |  |

|     |            |      |   |   |   |     |     |                   |                  |  |          |  |
|-----|------------|------|---|---|---|-----|-----|-------------------|------------------|--|----------|--|
| 697 | cg30384142 | 40   | CTTGCGCGGCA<br>CCAGGCGGTAA<br>GAC[G/A]ACCCA<br>TATTTAGAACT<br>GGCACCTC  | G | A | Thr | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P44788 SUN PROTEIN (FMU<br>PROTEIN) - Haemophilus influenzae,<br>451 aa.   | 5.30E-56 |  |
| 698 | cg44015614 | 1289 | GCTCTGGCTGG<br>GGTGCACTATA<br>CTT[C/T]TCCAC<br>GTATTCTATTTC<br>CACAACTT | C | T | Glu | Glu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P91343 HYPOTHETICAL 49.0<br>KD TRP-ASP REPEATS<br>CONTAINING PROTEIN F55F8.5 IN<br>CHROMOSOME I - Caenorhabditis<br>elegans, 439 aa. | 3.30E-54 |  |
| 699 | cg44015614 | 1295 | GCTGGGTGCA<br>GTAACTTCTCC<br>AC[G/A]TATTCTA<br>TTTCCACAACCT<br>CTTCTG   | G | A | Tyr | Tyr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P91343 HYPOTHETICAL 49.0<br>KD TRP-ASP REPEATS<br>CONTAINING PROTEIN F55F8.5 IN<br>CHROMOSOME I - Caenorhabditis<br>elegans, 439 aa. | 3.30E-54 |  |
| 700 | cg44015614 | 1313 | TCTCCACGTATT<br>CTATTTCCACAA<br>C[T/C]TCTTCTGA<br>TGAGATGTTCTC<br>CATT  | T | C | Glu | Glu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P91343 HYPOTHETICAL 49.0<br>KD TRP-ASP REPEATS<br>CONTAINING PROTEIN F55F8.5 IN<br>CHROMOSOME I - Caenorhabditis<br>elegans, 439 aa. | 3.30E-54 |  |
| 701 | cg44015614 | 1319 | CGTATTCTATT<br>CCACAACCTCTT<br>C[T/C]GATGAGA<br>TGTTCTCCATTT<br>CCATGT  | T | C | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P91343 HYPOTHETICAL 49.0<br>KD TRP-ASP REPEATS<br>CONTAINING PROTEIN F55F8.5 IN<br>CHROMOSOME I - Caenorhabditis<br>elegans, 439 aa. | 3.30E-54 |  |
| 702 | cg44015614 | 1325 | CTATTTCCACAA<br>CTTCTTCTGATG<br>A[G/A]ATGTTCTC<br>CATTTCATGTC<br>TTTGT  | G | A | Ile | Ile | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P91343 HYPOTHETICAL 49.0<br>KD TRP-ASP REPEATS<br>CONTAINING PROTEIN F55F8.5 IN<br>CHROMOSOME I - Caenorhabditis<br>elegans, 439 aa. | 3.30E-54 |  |

|     |            |      |  |   |   |     |     |                   |                  |  |          |    |
|-----|------------|------|--|---|---|-----|-----|-------------------|------------------|--|----------|----|
| 703 | cg44015614 | 1379 | AGGGCATTGCG<br>AGAAACTGGCC<br>CTT[A/G]ATAAG<br>GAAATCAAACCTC<br>CACATGTT | A | G | Ile | Ile | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P91343 HYPOTHETICAL 49.0<br>KD TRP-ASP REPEATS<br>CONTAINING PROTEIN F55F8.5 IN<br>CHROMOSOME I - Caenorhabditis<br>elegans, 439 aa. | 3.30E-54 |    |
| 704 | cg42380652 | 406  | AGTCCAGGCG<br>GGGCCACGTC<br>CTC[T/C]CGTA<br>CACCTTTCCAG<br>GAAGGGC       | T | C | Arg | Arg | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q62739 RABIN3 - RATTUS<br>NORVEGICUS (RAT), 460 aa.   | 4.20E-54 |    |
| 705 | cg43931038 | 425  | TCTTCTCTAGAG<br>TCCCGCGGCTC<br>AC[A/G]GCCTTT<br>GCTGCGAAGGG<br>CAACTTGT  | A | G | Ala | Ala | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O46082 EG:63B12.2 PROTEIN -<br>DROSOPHILA MELANOGASTER<br>(FRUIT FLY), 254 aa.  | 6.10E-54 | 11 |
| 706 | cg43931038 | 436  | GTCCCGCGGCT<br>CACAGCCTTTG<br>CTG[C/G]GAAGG<br>GCAACTTGTGG<br>GCAACCTGG  | C | G | Ser | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O46082 EG:63B12.2 PROTEIN -<br>DROSOPHILA MELANOGASTER<br>(FRUIT FLY), 254 aa.  | 6.10E-54 | 11 |
| 707 | cg43931038 | 463  | AAGGGCAACTT<br>GTGGGCAACCT<br>GGT[C/T]AAGGA<br>AACCTTGACTTC<br>TTCAAAT   | C | T | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O46082 EG:63B12.2 PROTEIN -<br>DROSOPHILA MELANOGASTER<br>(FRUIT FLY), 254 aa.  | 6.10E-54 | 11 |
| 708 | cg43931038 | 469  | AACTTGTGGGC<br>AACCTGGTCAA<br>GGA[A/C]ACCTT<br>GACTTCTTCAA<br>TTCACAAC   | A | C | Val | Val | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O46082 EG:63B12.2 PROTEIN -<br>DROSOPHILA MELANOGASTER<br>(FRUIT FLY), 254 aa.  | 6.10E-54 | 11 |
| 709 | cg43931038 | 478  | GCAACCTGGTC<br>AAGGAAACCTT<br>GACT[C/T]CTTCA<br>AATTCACAACGC<br>CCACCCA  | T | C | Glu | Glu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O46082 EG:63B12.2 PROTEIN -<br>DROSOPHILA MELANOGASTER<br>(FRUIT FLY), 254 aa.  | 6.10E-54 | 11 |

|     |            |     |   |   |   |     |     |                   |                  |   |          |    |
|-----|------------|-----|---|---|---|-----|-----|-------------------|------------------|---|----------|----|
| 710 | cg43931038 | 496 | CCTTGACTTCTT<br>CAAATTCACAAC<br>GIC/TJCCACCCA<br>TCTCTACAACAA<br>GGCGGC | C | T | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O46082 EG:63B12.2 PROTEIN -<br>DROSOPHILA MELANOGASTER<br>(FRUIT FLY), 254 aa.           | 6.10E-54 | 11 |
| 711 | cg43931038 | 562 | TCACGTAAGTGG<br>TCAATAGCACCT<br>TTIGAJCCTCCC<br>CCCATGCGATG<br>CCCAACAC | G | A | Gly | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O46082 EG:63B12.2 PROTEIN -<br>DROSOPHILA MELANOGASTER<br>(FRUIT FLY), 254 aa.           | 6.10E-54 | 11 |
| 712 | cg43338979 | 360 | CATCATCTCCTG<br>AAGATGCTAGC<br>AC[C/T]GTTTCT<br>GTTATATTCCAA<br>CTCACTC | C | T | Thr | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O45933 Y43F4B.4 -<br>CAENORHABDITIS ELEGANS, 363<br>aa.                                  | 1.40E-53 | 18 |
| 713 | cg38450437 | 104 | GAATTGGTTCTG<br>AGGAGTTTGG<br>GA[G/A]CTTCTTT<br>TACTGATGGACA<br>GAAATC  | G | A | Glu | Glu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O43168 KIAA0443 - HOMO<br>SAPIENS (HUMAN), 1395 aa.                                      | 3.50E-52 |    |
| 714 | cg38450437 | 47  | CCAGGGAAGT<br>GCACAGCCAGA<br>GAA[T/C]TGGTC<br>TTGCAACTGCAT<br>CCAGTGTG  | T | C | Asn | Asn | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O43168 KIAA0443 - HOMO<br>SAPIENS (HUMAN), 1395 aa.                                      | 3.50E-52 |    |
| 715 | cg43314946 | 458 | CCTTCCGGATG<br>ACTTCTCCGCA<br>TC[C/T]TGCCCC<br>AGCAGCTGGAC<br>AGCATACA  | C | T | Leu | Leu | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD37447 BAW -<br>FUGU RUBRIPES (JAPANESE<br>PUFFERFISH) (TAKIFUGU<br>RUBRIPES), 402 aa. | 1.60E-51 | 17 |
| 716 | cg44010070 | 320 | TCAAGCACTCG<br>GACGGGACGCG<br>CAC[T/C]TGCGC<br>CAAGCTCTATGA<br>CAAGAGCG | T | C | Thr | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:O35775 SYNCOLLIN (SIP9) -<br>Rattus norvegicus (Rat), 145 aa.                            | 6.40E-51 |    |



|     |            |     |   |   |   |     |                   |                   |  |           |  |
|-----|------------|-----|---|---|---|-----|-------------------|-------------------|--|-----------|--|
| 717 | cg39380052 | 563 | ACCTCATCACCC<br>CGTACCATCAG<br>AC[C/T]CTCGAC<br>AAGTCACTGA<br>GCGTTTTC    | C | T | Thr | SILENT-<br>CODING | UNCLAS<br>SIFIED  | Human Gene Similar to<br>TREMBLNEW-ACC:CAB42016<br>PUTATIVE ADENYLOSUCCINATE<br>SYNTHETASE - STREPTOMYCES<br>COELICOLOR, 427 aa. | 1.30E-50  |  |
| 718 | cg39380052 | 641 | GTCGTGGCATC<br>GGCCCGACCTA<br>CTC[T/C]GACAA<br>GATCAATCGGAT<br>GGTATTC    | T | C | Ser | SILENT-<br>CODING | UNCLAS<br>SIFIED  | Human Gene Similar to<br>TREMBLNEW-ACC:CAB42016<br>PUTATIVE ADENYLOSUCCINATE<br>SYNTHETASE - STREPTOMYCES<br>COELICOLOR, 427 aa. | 1.30E-50  |  |
| 719 | cg39380052 | 662 | ACTCTGACAAGA<br>TCAATCGGATG<br>GG[T/C]ATTGCG<br>GTCCAGGATCTT<br>TTGACG    | T | C | Gly | SILENT-<br>CODING | UNCLAS<br>SIFIED  | Human Gene Similar to<br>TREMBLNEW-ACC:CAB42016<br>PUTATIVE ADENYLOSUCCINATE<br>SYNTHETASE - STREPTOMYCES<br>COELICOLOR, 427 aa. | 1.30E-50  |  |
| 720 | cg43329819 | 585 | TCATCGACAACC<br>AGAACCTCCTCT<br>TT[C/G]AGCTCT<br>CCTACAAGCTG<br>GAGGCAA   | T | C | Phe | SILENT-<br>CODING | UNCLAS<br>SIFIED  | Human Gene Similar to SPTREMBL-<br>ACC:Q92565 MYELOBLAST<br>KIAA0277 - HOMO SAPIENS<br>(HUMAN), 580 aa.                          | 1.40E-50  |  |
| 721 | cg43298242 | 138 | CTGAAGATCTGT<br>TGACAGGGCTC<br>AC[A/G]GAGACG<br>GGGTGAGGGG<br>AGAGATCG    | A | G | Ser | SILENT-<br>CODING | water_ch<br>annel | Human Gene SWISSPROT-<br>ID:O14520 AQUAPORIN-7 LIKE<br>(AQUAPORIN ADIPOSE) (AQPAP) -<br>HOMO SAPIENS (HUMAN), 342 aa.            | 1.30E-163 |  |
| 722 | cg43298242 | 150 | TGGCAGGGGCTC<br>ACAGAGACGGG<br>GGT[G/A]AGGGG<br>AGAGATCGTGG<br>GTTTCATGAG | G | A | Leu | SILENT-<br>CODING | water_ch<br>annel | Human Gene SWISSPROT-<br>ID:O14520 AQUAPORIN-7 LIKE<br>(AQUAPORIN ADIPOSE) (AQPAP) -<br>HOMO SAPIENS (HUMAN), 342 aa.            | 1.30E-163 |  |

|     |            |      |   |   |   |     |               |                  |                           |   |           |               |
|-----|------------|------|---|---|---|-----|---------------|------------------|---------------------------|---|-----------|---------------|
| 723 | cg43970780 | 1501 | GGAGTTCTGGT<br>TCTGGTAGATG<br>GAA[G/A]CTTTCT<br>CTTTCAACAGGT<br>CCAGACA | G | A | Ala | Val<br>(1096) | CONSERVATI<br>VE | apoptosi<br>s             | Human Gene SWISSNEW-ID:Q92785<br>ZINC-FINGER PROTEIN UBI-D4<br>(APOPTOSIS RESPONSE ZINC<br>FINGER PROTEIN REQUIEM) -<br>HOMO SAPIENS (HUMAN), 391<br>aa.lpcis:SWISSPROT-ID:Q92785<br>ZINC-FINGER PROTEIN UBI-D4<br>(APOPTOSIS RESPONSE ZINC<br>FINGER PROTEIN REQUIEM) -<br>HOMO SAPIENS (HUMAN), 391 aa.   | 2.30E-212 | 11            |
| 724 | cg43957906 | 460  | GGAGTCCTTGG<br>CGGCGTCATAT<br>GGG[T/C]GCTCC<br>TTGGAGGGGAT<br>CTCCAGGAC | T | C | His | Arg<br>(1097) | CONSERVATI<br>VE | ATPase_<br>associat<br>ed | Human Gene Similar to SWISSPROT-<br>ID:Q16864 VACUOLAR ATP<br>SYNTHASE SUBUNIT F (EC<br>3.6.1.34) (V-ATPASE F SUBUNIT) (V-<br>ATPASE 14 KD SUBUNIT) - HOMO<br>SAPIENS (HUMAN), 119 aa.  | 2.20E-58  | 12            |
| 725 | cg43952088 | 2923 | TGAGGGGAGCG<br>TCGCCGGCCGC<br>GGA[G/A]CAGAT<br>GCCGCGGGGC<br>CGCTCGCAG  | G | A | Ala | Val<br>(1098) | CONSERVATI<br>VE | cadherin                  | Human Gene SPTREMBL-ID:Q15065<br>OB-CADHERIN-1 - HOMO SAPIENS<br>(HUMAN), 796 aa.   | 0.00E+00  | 16            |
| 726 | cg43956666 | 613  | ACTCCTGTTCTG<br>GGGACAGTTTG<br>GT[A/G]TTAAAC<br>ACTTAAATATAG<br>ATCCGG  | A | G | Ile | Val<br>(1099) | CONSERVATI<br>VE | cadherin                  | Human Gene SWISSNEW-ID:Q08722<br>LEUKOCYTE SURFACE ANTIGEN<br>CD47 PRECURSOR (ANTIGENIC<br>SURFACE DETERMINANT PROTEIN<br>OA3) (INTEGRIN ASSOCIATED<br>PROTEIN) (IAP) (MER6) - HOMO<br>SAPIENS (HUMAN), 323<br>aa.lpcis:SWISSPROT-ID:Q08722<br>LEUKOCYTE SURFACE ANTIGEN<br>CD47 PRECURSOR (ANTIGENIC<br>SURFACE DETERMINANT PROTEIN<br>OA3) (INTEGRIN ASSOCIATED<br>PROTEIN) (IAP) (MER6) - HOMO<br>SAPIENS (HUMAN), 323 aa. | 1.20E-167 | 3<br>(3q13.1) |

|     |            |      |  |   |   |     |               |                  |                    |   |           |               |
|-----|------------|------|--|---|---|-----|---------------|------------------|--------------------|---|-----------|---------------|
| 727 | cg43942011 | 1327 | TTCCCCCATGTGA<br>AACATCTGGCTT<br>G[C/T]GACAGGT<br>GATTTTTCACA<br>GGTAGG  | C | T | Arg | His<br>(1100) | CONSERVATI<br>VE | complem<br>entcept | Human Gene Similar to<br>TREMBLNEW-ID:E246058<br>COMPLEMENT RECEPTOR 2 - MUS<br>MUSCULUS (MOUSE), 651 aa<br>(fragment).   | 1.10E-69  | 1 (1q32)      |
| 728 | cg43973728 | 987  | TATGAACACCCC<br>AGATCTGAAGAA<br>GT[C/T]GCTGTT<br>CTGAAACAGAA<br>GTTGGAG  | T | C | Val | Ala<br>(1101) | CONSERVATI<br>VE | cyclin             | Human Gene SWISSPROT-<br>ID:P51946 CYCLIN H (MO15-<br>ASSOCIATED PROTEIN) (P37) (P34)<br>- HOMO SAPIENS (HUMAN), 323 aa.  | 2.60E-172 | 5<br>(5q13.3) |
| 729 | cg44017721 | 291  | TCCTGCTCCTCC<br>GTGGCCTCCTTT<br>G[G/A]CAGCGCT<br>GGCCAAGCCCC<br>GGGTCAG  | G | A | Ala | Val<br>(1102) | CONSERVATI<br>VE | cytochro<br>me     | Human Gene Similar to SPTREMBL-<br>ID:O00761 CYTOCHROME<br>OXIDASE SUBUNIT VIA HEART<br>ISOFORM PRECURSOR (EC 1.9.3.1)<br>(CYTOCHROME-C OXIDASE)<br>(CYTOCHROME A(3))<br>(CYTOCHROME AA(3)) - HOMO<br>SAPIENS (HUMAN), 97 aa. | 2.40E-52  | 22            |
| 730 | cg43273880 | 5428 | CAAAAAGAGAAA<br>GACGACGTGAC<br>TG[G/C]GGGTAA<br>GAAACCATTTTCG<br>TCCAGAG | G | C | Gly | Ala<br>(1103) | CONSERVATI<br>VE | dna_rna<br>_bind   | Human Gene SWISSPROT-<br>ID:O14647 CHROMODOMAIN-<br>HELICASE-DNA-BINDING PROTEIN<br>2 (CHD-2) - HOMO SAPIENS<br>(HUMAN), 1739 aa.   | 0.00E+00  | 15            |
| 731 | cg43992911 | 485  | GAAGAGAACTT<br>TTTTAAACTGAA<br>C[A/G]ATAAAAG<br>TGAAAAAGATAA<br>GAAGGA   | A | G | Asn | Asp<br>(1104) | CONSERVATI<br>VE | glycoprot<br>ein   | Human Gene SWISSPROT-<br>ID:P08183 MULTIDRUG<br>RESISTANCE PROTEIN 1 (P-<br>GLYCOPROTEIN 1) - HOMO<br>SAPIENS (HUMAN), 1280 aa.   | 0.00E+00  | 7             |
| 732 | cg41029366 | 890  | TGCGGCCACAA<br>AGAGGACGCGG<br>GCGT[C]GGTGT<br>GCTCAGAGCAC<br>CAGTCCTGG   | T | C | Val | Ala<br>(1105) | CONSERVATI<br>VE | glycoprot<br>ein   | Human Gene SPTREMBL-ID:Q61003<br>T CELL SURFACE GLYCOPROTEIN<br>CD6 - MUS MUSCULUS (MOUSE),<br>665 aa.  | 1.00E-234 | 11            |

|     |            |      |   |   |   |     |               |                  |                |   |           |   |
|-----|------------|------|---|---|---|-----|---------------|------------------|----------------|---|-----------|---|
| 733 | cg43931167 | 2546 | CGAGAACTGAA<br>GAAAGCAAGAA<br>CAGT/GJCCTAC<br>AAATGGATGAAC<br>TCAAATGT  | T | G | Val | Gly<br>(1106) | CONSERVATI<br>VE | helicase       | Human Gene SWISSPROT-<br>ID:O14232 PUTATIVE HELICASE<br>C6F12.16 IN CHROMOSOME I -<br>SCHIZOSACCHAROMYCES POMBE<br>(FISSION YEAST), 1117 aa.  | 3.30E-307 | 5 |
| 734 | cg43925670 | 2360 | AATCTGAATTTT<br>GTCATACTCTTC<br>T[C/T]TCATTTT<br>AAATTAAGTTT<br>AAATC   | C | T | Arg | Lys<br>(1107) | CONSERVATI<br>VE | interfero<br>n | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.lpcsl:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0.00E+00  | 1 |
| 735 | cg43925670 | 2474 | TAGAACAAATGTT<br>CTTGATTTTTTT<br>[C/G]CCATCTTTA<br>CAGACATAAGT<br>GAGCC | C | G | Gly | Ala<br>(1108) | CONSERVATI<br>VE | interfero<br>n | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.lpcsl:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0.00E+00  | 1 |

|     |            |      |  |   |   |     |               |                  |        |   |           |    |
|-----|------------|------|--|---|---|-----|---------------|------------------|--------|---|-----------|----|
| 736 | cg43928549 | 4637 | AATTGGCACATC<br>TTGGCGCGAAA<br>GT[C/T]GTTCAC<br>TCTGGGTCGCA<br>CAAGGAG | C | T | Asp | Asn<br>(1109) | CONSERVATI<br>VE | kinase | Human Gene SWISSNEW-ID:O00329<br>PHOSPHATIDYLINOSITOL 3-<br>KINASE CATALYTIC SUBUNIT,<br>DELTA ISOFORM (EC 2.7.1.137)<br>(PI3-KINASE P110 SUBUNIT DELTA)<br>(PTDINS-3-KINASE P110) (PI3K)<br>(P110DELTA) - HOMO SAPIENS<br>(HUMAN), 1044<br>aa.lpcis:SWISSPROT-ID:O00329<br>PHOSPHATIDYLINOSITOL 3-<br>KINASE CATALYTIC SUBUNIT,<br>DELTA ISOFORM (EC 2.7.1.137)<br>(PI3-KINASE P110 SUBUNIT DELTA)<br>(PTDINS-3-KINASE P110) (PI3K)<br>(P110DELTA) - HOMO SAPIENS<br>(HUMAN), 1044 aa.lpcis:SPTREMBL-<br>ID:O00329 PHOSPHOINOSITIDE 3-<br>KINASE - HOMO SAPIENS<br>(HUMAN), 1044 aa. | 0.00E+00  |    |
| 737 | cg42703622 | 409  | GAAGAAGGAAT<br>TTGGAGGTGGC<br>CAC[A/G]TTAA<br>GATGAAGTATTT<br>GGAACAGT | A | G | Ile | Val<br>(1110) | CONSERVATI<br>VE | kinase | Human Gene SPTREMBL-ID:Q12792<br>PROTEIN TYROSINE KINASE -<br>HOMO SAPIENS (HUMAN), 350 aa.   | 3.00E-187 | 12 |
| 738 | cg44131752 | 925  | CTCTGCGTGCT<br>CGTCCCGAAGT<br>GAC[C/G]TGCCT<br>GGTCCGACAA<br>GGACACTGA | C | G | Leu | Val<br>(1111) | CONSERVATI<br>VE | kinase | Human Gene SPTREMBL-ID:Q15599<br>TYROSINE KINASE ACTIVATOR<br>PROTEIN 1 (TKA-1) - HOMO<br>SAPIENS (HUMAN), 450 aa.  | 7.80E-173 | 16 |
| 739 | cg25143358 | 394  | CAGGTGGCCAT<br>TCGGCGCGCTT<br>CAA[G/T]TTTCGT<br>GGTCATGCCCG<br>CGGTTC  | G | T | Leu | Ile<br>(1112) | CONSERVATI<br>VE | kinase | Human Gene Similar to SWISSPROT-<br>ID:P46546 GLUTAMATE 5-KINASE<br>(EC 2.7.2.11) (GAMMA-GLUTAMYL<br>KINASE) (GK) -<br>CORYNEBACTERIUM<br>GLUTAMICUM, 369 aa.   | 2.70E-51  |    |

|     |            |     |   |   |   |     |               |                  |                     |  |          |   |
|-----|------------|-----|---|---|---|-----|---------------|------------------|---------------------|--|----------|---|
| 740 | cg43105476 | 702 | GCGAAACAGT<br>TCGGTCTTTCAA<br>AT[C/T]GGGATT<br>AGCACCTCTAA<br>GTAGCAGT    | C | T | Asp | Asn<br>(1113) | CONSERVATI<br>VE | kinase<br>inhibitor | Human Gene Similar to SWISSPROT-<br>ID:P42773 CYCLIN-DEPENDENT<br>KINASE 6 INHIBITOR (P18-INK6) -<br>HOMO SAPIENS (HUMAN), 168 aa.   | 7.80E-86 |   |
| 741 | cg38642684 | 290 | ATATTGCCCTAGT<br>AATTTCTGATAA<br>T[C/T]ATTAAAGG<br>TATGTAAGTTGC<br>TAGTA  | C | T | Asp | Asn<br>(1114) | CONSERVATI<br>VE | nuclease            | Human Gene Similar to SWISSNEW-<br>ID:P10266 RETROVIRUS-RELATED<br>POLYPROTEIN [CONTAINS:<br>REVERSE TRANSCRIPTASE (EC<br>2.7.7.49); ENDONUCLEASE] -<br>HOMO SAPIENS (HUMAN), 874<br>aa.   pcis:SWISSPROT-ID:P10266<br>RETROVIRUS-RELATED POLY<br>PROTEIN (REVERSE<br>TRANSCRIPTASE (EC 2.7.7.49);<br>ENDONUCLEASE) - HOMO<br>SAPIENS (HUMAN), 874 aa. | 2.60E-50 |   |
| 742 | cg39518465 | 864 | CACCTTCTCTAAAG<br>GAGATGAAGGA<br>AG[C/T]CCTGGG<br>CACCCCTGGCG<br>CAGCCAAT | C | T | Ala | Val<br>(1115) | CONSERVATI<br>VE | oncogen<br>e        | Human Gene SWISSPROT-<br>ID:P15498 VAV PROTO-ONCOGENE<br>- HOMO SAPIENS (HUMAN), 846 aa.   | 0.00E+00 |   |
| 743 | cg43021380 | 176 | CAGCCGCCCGG<br>GGGGCTGCAGC<br>GCC[G/A]TTAGT<br>GCCACGCGCTG<br>TCTATTGTA   | G | A | Val | Ile<br>(1116) | CONSERVATI<br>VE | phosphat<br>ase     | Human Gene SWISSPROT-<br>ID:Q16849 PROTEIN-TYROSINE<br>PHOSPHATASE N PRECURSOR<br>(EC 3.1.3.48) (R-PTP-N) (PTP IA-2)<br>(ISLET CELL ANTIGEN 512) (ICA<br>512) (ISLET CELL AUTOANTIGEN 3)<br>- HOMO SAPIENS (HUMAN), 979 aa.  | 0.00E+00 | 2 |
| 744 | cg39728924 | 365 | CAATTGTGGAG<br>AAGAGTATTTTT<br>AT[G/A]TCGCTA<br>CTCAAGGACCA<br>CTGCTGAG   | G | A | Val | Ile<br>(1117) | CONSERVATI<br>VE | phosphat<br>ase     | Human Gene Similar to<br>TREMBLNEW-ID:D1024666<br>PROTEIN-TYROSINE-<br>PHOSPHATASE (EC 3.1.3.48) - MUS<br>MUSCULUS (MOUSE), 426 aa.  | 1.20E-64 |   |

|     |            |      |  |   |   |     |               |                  |                |  |           |                     |
|-----|------------|------|--|---|---|-----|---------------|------------------|----------------|--|-----------|---------------------|
| 745 | cg42710490 | 851  | CAACACAGCCTAT<br>TGCGGGAAGAA<br>AT[G/A]TCCAGG<br>GTGGAATCCGT<br>TTTGGGGA | G | A | Val | Ile<br>(1118) | CONSERVATI<br>VE | polymera<br>se | Human Gene SWISSNEW-ID:O54888<br>DNA-DIRECTED RNA<br>POLYMERASE I 135 KD<br>POLYPEPTIDE (EC 2.7.7.6) (RNA<br>POLYMERASE I SUBUNIT 2)<br>(RPA135) (RNA POLYMERASE I 127<br>KD SUBUNIT) - RATTUS<br>NORVEGICUS (RAT), 1135<br>aa.lpcis:TREMBLNEW-ID:G2739048<br>RNA POLYMERASE I 127 KDA<br>SUBUNIT - RATTUS NORVEGICUS<br>(RAT), 1135 aa. | 8.90E-172 |                     |
| 746 | cg44001078 | 316  | GGTTATCAGGA<br>ACTTGGGATCTT<br>CA[C/T]GGATTT<br>CCATCTTGTTCT<br>TCATCCA  | C | T | Arg | His<br>(1119) | CONSERVATI<br>VE | struct         | Human Gene TREMBLNEW-<br>ID:G2920823 CARDIAC MYOSIN<br>BINDING PROTEIN-C - HOMO<br>SAPIENS (HUMAN), 1274 aa.   | 0.00E+00  |                     |
| 747 | cg43916919 | 1113 | AGGTAGGAGTC<br>CCCCGAGAAGA<br>AGA[C/T]GCCCT<br>GGTTCTCTTGC<br>GCCACAGGC  | C | T | Val | Ile<br>(1120) | CONSERVATI<br>VE | struct         | Human Gene SWISSNEW-ID:P40121<br>MACROPHAGE CAPPING PROTEIN<br>(ACTIN-REGULATORY PROTEIN<br>CAP-G) - HOMO SAPIENS (HUMAN),<br>348 aa.lpcis:SWISSPROT-ID:P40121<br>MACROPHAGE CAPPING PROTEIN<br>(ACTIN-REGULATORY PROTEIN<br>CAP-G) - HOMO SAPIENS (HUMAN),<br>348 aa.   | 4.3E-188  | 2 (2cen)            |
| 748 | cg42930605 | 463  | CAGCTCCTTGCT<br>GGTCTTCTGCA<br>CC[C/T]TCACCT<br>CCATGTCGTACT<br>TCTCCTC  | C | T | Arg | Lys<br>(1121) | CONSERVATI<br>VE | struct         | Human Gene Similar to SWISSPROT-<br>ID:P48788 TROPONIN I, FAST<br>SKELETAL MUSCLE (TROPONIN I,<br>FAST-TWITCH ISOFORM) - HOMO<br>SAPIENS (HUMAN), 181 aa.  | 1E-92     | 11<br>(11p15.5<br>) |
| 749 | cg36824552 | 230  | AAGACGAGCCG<br>AGGCTTCACCTA<br>CC[A/G]CCTGCA<br>CTTCTGGCTCG<br>GAAAGGAG  | A | G | His | Arg<br>(1122) | CONSERVATI<br>VE | struct         | Human Gene Similar to SWISSPROT-<br>ID:Q28046 ADSEVERIN<br>(SCINDERIN) (SC) - BOS TAURUS<br>(BOVINE), 715 aa.  | 4E-80     |                     |

|     |            |      |  |   |   |     |               |                  |                      |  |          |   |
|-----|------------|------|--|---|---|-----|---------------|------------------|----------------------|--|----------|---|
| 750 | cg42522566 | 377  | CAACATCATGAA<br>CCAGCTCAGCC<br>AC[G/A]TAAACTT<br>GATCCAACCTTTA<br>TGATGC | G | A | Val | Ile<br>(1123) | CONSERVATI<br>VE | struct               | Human Gene Similar to SWISSPROT-<br>ID:P07313 MYOSIN LIGHT CHAIN<br>KINASE, SKELETAL MUSCLE (EC<br>2.7.1.117) (MLCK) - ORYCTOLAGUS<br>CUNICULUS (RABBIT), 607 aa.  | 6E-55    |   |
| 751 | cg42522566 | 509  | GTACCACTCA<br>CTGAGTTGGAT<br>GTG[G/A]TCTTG<br>TTCACGAGGCA<br>GATCTGTGA   | G | A | Val | Ile<br>(1124) | CONSERVATI<br>VE | struct               | Human Gene Similar to SWISSPROT-<br>ID:P07313 MYOSIN LIGHT CHAIN<br>KINASE, SKELETAL MUSCLE (EC<br>2.7.1.117) (MLCK) - ORYCTOLAGUS<br>CUNICULUS (RABBIT), 607 aa.  | 6E-55    |   |
| 752 | cg42489842 | 481  | TGCAAGTGAATA<br>TGCCAAATACTG<br>CTT[A/C]AGAAATA<br>TTAGGAGTTGCA<br>GCTAC | T | A | Ser | Thr<br>(1125) | CONSERVATI<br>VE | tm7                  | Human Gene Homologous to<br>SWISSPROT-ID:Q02038<br>NEUROLYSIN PRECURSOR (EC<br>3.4.24.16) (NEUROTENSIN<br>ENDOPEPTIDASE)<br>(MITOCHONDRIAL<br>OLIGOPEPTIDASE M)<br>(MICROSOMAL ENDOPEPTIDASE)<br>(MEP) (SOLUBLE ANGIOTENSIN-<br>BINDING PROTEIN) (SABP) - SUS<br>SCROFA (PIG), 704 aa. | 7.3E-106 |   |
| 753 | cg43919398 | 2201 | GTTAGTCTCTGT<br>GGTGTGCTTATA<br>A[T/C]CATTTGG<br>GGTCCAACATTG<br>ACATTT  | T | C | Ile | Val<br>(1126) | CONSERVATI<br>VE | transcript<br>factor | Human Gene SWISSPROT-<br>ID:Q14188 TRANSCRIPTION<br>FACTOR DP-2 (E2F DIMERIZATION<br>PARTNER 2) - HOMO SAPIENS<br>(HUMAN), 385 aa.   | 2.7E-202 | 3 |
| 754 | cg20612302 | 300  | ATGGAGGCGGC<br>CCACATGGCGG<br>CCA[C/G]CGCCA<br>TCCTCAACCTGT<br>CCACGCGC  | C | G | Thr | Ser<br>(1127) | CONSERVATI<br>VE | transcript<br>factor | Human Gene Similar to SPTREMBL-<br>ID:O08996 MYELIN<br>TRANSCRIPTION FACTOR 1-LIKE -<br>MUS MUSCULUS (MOUSE), 1182<br>aa.  | 1.7E-53  |   |
| 755 | cg44928196 | 1474 | GGCTCTGTTCC<br>ATGGGAAATTCA<br>TA[G/A]ACACGG<br>GTTTTCTTTAC<br>CATTCTA   | G | A | Asp | Asn<br>(1128) | CONSERVATI<br>VE | ubiquitin            | Human Gene TREMBLNEW-<br>ID:G2827198 UBIQUITIN PROTEIN<br>LIGASE - MUS MUSCULUS<br>(MOUSE), 854 aa.  | 0        |   |



|     |            |      |  |   |   |     |               |                  |                  |   |           |    |
|-----|------------|------|--|---|---|-----|---------------|------------------|------------------|---|-----------|----|
| 756 | cg43301812 | 3784 | GGCTGGTCCTT<br>CTCCATGGCTG<br>GGATTCGCTCT<br>GCTGGCCTTGG<br>TTTTGCCCG    | T | C | His | Arg<br>(1129) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:Q93075 HYPOTHETICAL<br>PROTEIN KIAA0218 - Homo sapiens<br>(Human), 761 aa.   | 0.00E+00  | 3  |
| 757 | cg43917191 | 2735 | GCTTCTCTTTTC<br>ACATTGTATGTA<br>TTCCTCAGGTGT<br>TCTTGCAACTCC<br>AAAAACA  | C | T | Asp | Asn<br>(1130) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAAT4849 KIAA0826 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1236 aa<br>(fragment).  | 0.00E+00  | 4  |
| 758 | cg43918356 | 2637 | GCTCATGTCATC<br>TTCATCTAGAAA<br>C[G/A]CCCTCAC<br>GGAAATGGAATT<br>GCTGCC  | G | A | Ala | Val<br>(1131) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75176 KIAA0692 PROTEIN -<br>HOMO SAPIENS (HUMAN), 783 aa<br>(fragment).  | 0.00E+00  | 12 |
| 759 | cg43932090 | 1186 | TCCTTTCAAGCT<br>TTCTTTATGTTG<br>TTTCCTATTGCT<br>TCATTTCTTGA<br>AGGTC     | T | C | Lys | Arg<br>(1132) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O00566 M PHASE<br>PHOSPHOPROTEIN 10 - HOMO<br>SAPIENS (HUMAN), 672 aa<br>(fragment).  | 0.00E+00  |    |
| 760 | cg43950437 | 794  | AGCCAGAGGCT<br>GGTACCTAGAA<br>CCA[G/C]TGGAT<br>GGTTCTTGGCT<br>GATGGCGC   | G | C | Thr | Ser<br>(1133) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q15021 ORF - HOMO SAPIENS<br>(HUMAN), 1401 aa.  | 0.00E+00  | 12 |
| 761 | cg42935995 | 743  | GCCTCGCTCCC<br>CGTCTGAGAGC<br>CTC[A/G]CGCCC<br>TCCAGCCAGCC<br>GTCACCTGCT | A | G | Val | Ala<br>(1134) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q12774 PROBABLE GUANINE<br>NUCLEOTIDE REGULATORY<br>PROTEIN TIM (ONCOGENE TIM)<br>(P60 TIM) (TRANSFORMING<br>IMMORTALIZED MAMMARY<br>ONCOGENE) - Homo sapiens<br>(Human), 519 aa. | 1.00E-274 |    |
| 762 | cg43971614 | 2578 | TCCATTGTAATC<br>CAATCCCCCAT<br>GG[A/G]CATAAG<br>AAGAGTCTTTTC<br>CATAAA   | A | G | Val | Ala<br>(1135) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13283 GAP SH3 BINDING<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 466 aa.  | 5.30E-253 | 5  |

|     |            |      |  |   |   |     |               |                  |                  |  |           |               |
|-----|------------|------|--|---|---|-----|---------------|------------------|------------------|--|-----------|---------------|
| 763 | cg43922856 | 1581 | CTTGAAATTTC<br>AGTCACCCCTATT<br>G[A/G]CAACTAA<br>GGATTCTGTTGCT<br>TGAAGC | A | G | Val | Ala<br>(1136) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P42167 THYMOPOIETINS<br>BETA AND GAMMA (TP BETA AND<br>TP GAMMA) - Homo sapiens<br>(Human), 453 aa.               | 2.00E-237 | 12<br>(12q22) |
| 764 | cg43922856 | 1783 | CCACTTGTCCT<br>TCAGTCTCAGTT<br>A[T/C]TCCAGCTT<br>GAGAATAGCTCT<br>GATTG   | T | C | Ile | Val<br>(1137) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P42167 THYMOPOIETINS<br>BETA AND GAMMA (TP BETA AND<br>TP GAMMA) - Homo sapiens<br>(Human), 453 aa.               | 2.00E-237 | 12<br>(12q22) |
| 765 | cg43955639 | 282  | GGCCGCGGG<br>GGATAGCTGCC<br>CAGG[C/G]TCAG<br>GAGGCTCTTG<br>GCTCCTGCCA    | C | G | Ser | Thr<br>(1138) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O15417 CAGL79 - HOMO<br>SAPIENS (HUMAN), 413 aa<br>(fragment).   | 2.80E-215 |               |
| 766 | cg41022625 | 1121 | CACGGCGTTCT<br>GGATCGTCTTCT<br>CC[A/G]TCAATC<br>ACATCATCGCCA<br>CCCTGCT  | A | G | Ile | Val<br>(1139) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD34036 CGI-40 PROTEIN -<br>HOMO SAPIENS (HUMAN), 845 aa.  | 2.00E-207 | 11            |
| 767 | cg43119894 | 1960 | TGAGCATAGCT<br>CTGAGCTCTCTT<br>TA[C/T]ACGGTC<br>AGGGTCCACAT<br>AATGCATT  | C | T | Val | Ile<br>(1140) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:CAA75235<br>LACTOSYL CERAMIDE ALPHA-2,3-<br>SIALYLTRANSFERASE (EC 2.4.99.9)<br>- MUS MUSCULUS (MOUSE), 387<br>aa. | 2.30E-190 | 2             |
| 768 | cg43303845 | 1109 | AGAACGAGAGA<br>GGCTGGAGAGA<br>CTG[C/G]AACGG<br>GAGAGGCAAGA<br>AAGGGAGCG  | C | G | Gln | Glu<br>(1141) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O93263 AVENA -<br>GALLUS GALLUS (CHICKEN), 550<br>aa.   | 1.90E-138 |               |
| 769 | cg44927166 | 531  | GTCCTTGTCTC<br>CCAATCCCTTTG<br>G[C/T]GTTCTCG<br>TTCCTTATCCCT<br>TTCCTCT  | C | T | Arg | His<br>(1142) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:BAA74876<br>KIAA0853 PROTEIN - HOMO<br>SAPIENS (HUMAN), 967 aa<br>(fragment).                        | 3.70E-133 | 13            |

|     |            |      |  |   |   |     |               |                  |                  |   |           |                |
|-----|------------|------|--|---|---|-----|---------------|------------------|------------------|---|-----------|----------------|
| 770 | cg38059286 | 473  | AGCTGTATAGCT<br>CCAGTGGTCCT<br>GA[G/T]CTCCGC<br>CGCTCCCTCTTC<br>TCACTGA  | G | T | Glu | Asp<br>(1143) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAD39906<br>FH1/FH2 DOMAIN-CONTAINING<br>PROTEIN FHOS - HOMO SAPIENS<br>(HUMAN), 1164 aa.   | 4.00E-129 |                |
| 771 | cg29351416 | 333  | CTGCCAGCCA<br>GCCCATCCCC<br>TGA[G/T]GACCT<br>GGCTTGTCAT<br>GGGCACCA      | G | T | Glu | Asp<br>(1144) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q03626 ALPHA-1-<br>INHIBITOR III PRECURSOR,<br>ISOFORM 2 (RAT PLASMA<br>PROTEINASE INHIBITOR ALPHA-1-<br>INHIBITOR III GROUP 3 VARIANT<br>36A) (ALPHA-1 PROTEINASE<br>INHIBITOR 3, EXONS 1-4) - RATTUS<br>NORVEGICUS (RAT), 1487 aa. | 3.20E-127 |                |
| 772 | cg43960639 | 987  | CCATGTCTGGG<br>AGAATGGGAGC<br>CTC[A/C]TCGCC<br>CACTTGAAGTC<br>AAAGTAGA   | A | C | Asp | Glu<br>(1145) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:CAB0416 P24B<br>PROTEIN PRECURSOR - HOMO<br>SAPIENS (HUMAN), 217 aa.  | 9.00E-111 |                |
| 773 | cg43325007 | 1098 | GTGGATATATGT<br>GGCCTGCAGTA<br>TG[G/A]CCACACA<br>GCTTCTCCTGG<br>AGGCTGCC | G | A | Ala | Val<br>(1146) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAD43195<br>PEROXISOMAL MEMBRANE<br>PROTEIN PMP 24 - HOMO SAPIENS<br>(HUMAN), 212 aa.   | 4.80E-110 | 20             |
| 774 | cg42907145 | 853  | GCCACCTCCCA<br>TAACCTTCTCAG<br>CA[G/A]CATAGA<br>CTGACTTGCCA<br>CATCGAGG  | G | A | Ala | Val<br>(1147) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSPROT-ACC:P50461 LIM<br>DOMAIN PROTEIN, CARDIAC<br>(MUSCLE LIM PROTEIN)<br>(CYSTEINE-RICH PROTEIN 3)<br>(CRP3) (LIM-ONLY PROTEIN 4) -<br>Homo sapiens (Human), 194 aa.  | 1.10E-108 | 11             |
| 775 | cg43972159 | 1374 | AAGCCATTAGGT<br>TCTCGGGCTGC<br>TGA/TIACGTGTC<br>GATTTGACTTT<br>TCITTC    | A | T | Ser | Thr<br>(1148) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q13845 BCL7B<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 202 aa.   | 2.60E-102 | 7<br>(12q24.1) |

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| 776 | cg39512856 | 508 | CCAGGGCTGTGC<br>CGTTCCACTTCT<br>GAT/AJATTCCC<br>CTCCCGGCGAT<br>AACCAGGT  | T | A | Tyr | Phe<br>(1149) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.   | 1.20E-98 |               |
| 777 | cg28461713 | 584 | TCTGCAAAITTTG<br>CTCCTGGGCAT<br>GG[G/A]CAGCTT<br>GCAGCTGAAGT<br>TGGTTGTA | G | A | Ala | Val<br>(1150) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P47710 ALPHA-S1 CASEIN<br>PRECURSOR - Homo sapiens<br>(Human), 185 aa.   | 5.90E-96 | 4<br>(4q21.1) |
| 778 | cg43969092 | 361 | CGGCGCCCGTC<br>ATCACGGATGT<br>GCA[C/A]GTCCC<br>CGTCGGTCAGC<br>AGCAGCACA  | C | A | Val | Leu<br>(1151) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA74913<br>KIAA0890 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1194 aa.  | 6.30E-89 |               |
| 779 | cg42688841 | 487 | GGTCATAGTAT<br>AAAGAAGGCTT<br>GA[C/T]GACAAA<br>CAGTCTCTTGCC<br>ATGGTCC   | C | T | Val | Ile<br>(1152) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:Q02380 NADH-UBIQUINONE<br>OXIDOREDUCTASE SGD<br>SUBUNIT PRECURSOR (EC 1.6.5.3)<br>(EC 1.6.99.3) (COMPLEX I-SGDH)<br>(CI-SGDH) - Bos taurus (Bovine), 189<br>aa. | 1.90E-83 |               |
| 780 | cg39523553 | 603 | GACGCGTTGGT<br>TCCCGACGAAG<br>ACG[C/T]CCGAG<br>CGGCCAAGTGG<br>GCGGTGGCG  | C | T | Ala | Val<br>(1153) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa.   | 7.20E-75 |               |
| 781 | cg39523553 | 819 | ATGGACGTGGT<br>GCGCAACAGCC<br>CTC[A/G]CGGAG<br>TGAAGGTCCAG<br>ATGGCTCTT  | A | G | His | Arg<br>(1154) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa.   | 7.20E-75 |               |

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| 782 | cg39523553 | 857  | CCAGATGGCTC<br>TTTCCGCCTGG<br>CCC[G/C]AGCTC<br>GATCAGGCATC<br>AAGGTGCCT  | G | C | Glu | Gln<br>(1155) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa.                | 7.20E-75 |    |
| 783 | cg35933325 | 274  | AACCACAGAGA<br>ATACAGTGACAA<br>CAJA/TJAGAAAC<br>AAATGACCAAA<br>TGCCACT   | A | T | Phe | Tyr<br>(1156) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA74845<br>KIAA0822 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1581 aa.                                 | 2.40E-74 |    |
| 784 | cg41677120 | 544  | GTTGTTTAACTT<br>AAGCAATTTTT<br>G[G/A]ATAAAAG<br>TGGATTGCAAG<br>GATATGA   | G | A | Asp | Asn<br>(1157) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q13492 CALM (TYPE I CALM<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 652 aa.                          | 1.10E-71 | 11 |
| 785 | cg43951096 | 2850 | AACATCAACAAT<br>CGTTATTGGGTC<br>TT[C/T]ATTTTGG<br>CTAGAAGAAAGTA<br>TCTGG | T | C | Lys | Arg<br>(1158) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q23382 ZK1058.4 -<br>CAENORHABDITIS ELEGANS, 442<br>aa.  | 2.00E-71 | 17 |
| 786 | cg42696021 | 444  | GCTGTGCCGCC<br>TTCACAATGAAG<br>TG[A/G]ACCGGA<br>AGCTGGGCAAG<br>CCTGATTT  | A | G | Asn | Asp<br>(1159) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P55789 AUGMENTER OF<br>LIVER REGENERATION (HERV1<br>PROTEIN) - Homo sapiens (Human),<br>125 aa. | 1.40E-69 |    |
| 787 | cg34243633 | 447  | GCTGGCACCGA<br>CATAAGAACTTG<br>TT[T/C]TCCAGCT<br>GGGGAGCAGCA<br>TGGCAAC  | T | C | Lys | Arg<br>(1160) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O88552 CLAUDIN-2 - MUS<br>MUSCULUS (MOUSE), 230 aa.  | 1.30E-68 |    |
| 788 | cg34243633 | 472  | TCCAGCTGGG<br>GAGCAGCATGG<br>CAA[C/T]CAGTG<br>TGCCCCAAAAGC<br>CCCAGAAAGG | C | T | Val | Ile<br>(1161) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O88552 CLAUDIN-2 - MUS<br>MUSCULUS (MOUSE), 230 aa.  | 1.30E-68 |    |

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|-----|------------|------|---|---|---|-----|---------------|------------------|------------------|--|----------|----------|
| 789 | cg43942922 | 268  | GTCCTCTGTCAA<br>GACCCCTGAAA<br>CA[G/A]TTGTCC<br>CCACAGCCCT<br>GAGCTCCA  | G | A | Val | Ile<br>(1162) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14676 KIAA0170 PROTEIN -<br>HOMO SAPIENS (HUMAN), 2089 aa.   | 2.30E-68 |          |
| 790 | cg43942922 | 310  | TGAGCTCCAGC<br>CTTCCACCTCCA<br>CA[G/A]ACCAGC<br>CTGTCACCTCTG<br>AGCCAC  | G | A | Asp | Asn<br>(1163) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14676 KIAA0170 PROTEIN -<br>HOMO SAPIENS (HUMAN), 2089 aa.   | 2.30E-68 |          |
| 791 | cg44938009 | 1139 | TTCTGTCAATGT<br>GGTCCGTGCCA<br>TG[A/G]TTGATAA<br>CTGGGATGTCC<br>TCTTCCA | A | G | Ile | Val<br>(1164) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:Q43182 RHO-GTPASE-<br>ACTIVATING PROTEIN 6 (RHO-<br>TYPE GTPASE-ACTIVATING<br>PROTEIN RHOGAPX-1) - Homo<br>sapiens (Human), 587 aa. | 5.80E-66 | X        |
| 792 | cg39516123 | 631  | AGCCCTCAGGC<br>GCGCCACAGAA<br>CAG[T/G]GGGCA<br>CCAACACTCCC<br>CCTAGTCCT | T | G | Val | Gly<br>(1165) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q04205 TENSIN - Gallus gallus<br>(Chicken), 1744 aa.   | 5.10E-62 |          |
| 793 | cg44921974 | 279  | GATTATGTCGCC<br>GTTGAGTTCGG<br>TC[A/G]CAGACT<br>TGATGTTTTGA<br>AAGTTGT  | A | G | Val | Ala<br>(1166) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P07148 FATTY ACID-BINDING<br>PROTEIN, LIVER (L-FABP) - Homo<br>sapiens (Human), 127 aa.  | 1.6E-61  | 2 (4q28) |
| 794 | cg42731307 | 497  | AAGGCATTGAT<br>GATCCGGTCCC<br>CCA[G/C]TGGGT<br>TGATGGCAAGTT<br>CTGGAATC | G | C | Leu | Val<br>(1167) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q99653 CALCIUM-BINDING<br>PROTEIN P22 (CALCIUM-BINDING<br>PROTEIN CHP) - Homo sapiens<br>(Human), 194 aa.                          | 2.60E-61 |          |
| 795 | cg42731307 | 534  | CAAGTTCTGGAAT<br>TCCTCTGGAAT<br>C[T/G]TCCCGGC<br>TGAGAGTCCCA<br>TTCTCTC | T | G | Glu | Asp<br>(1168) | CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q99653 CALCIUM-BINDING<br>PROTEIN P22 (CALCIUM-BINDING<br>PROTEIN CHP) - Homo sapiens<br>(Human), 194 aa.                          | 2.60E-61 |          |

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| 796 | cg44015614 | 1330 | TCCACAACCTCT<br>TCTGATGAGATG<br>TTTCCTCCATTT<br>CCATGTGTTTGT<br>CCAAG    | T | C | Asn | Asp<br>(1169) | CONSERVATI<br>VE         | UNCLAS<br>SIFIED          | Human Gene Similar to SWISSPROT-<br>ACC:P91343 HYPOTHETICAL 49.0<br>KD TRP-ASP REPEATS<br>CONTAINING PROTEIN F55F8.5 IN<br>CHROMOSOME I - Caenorhabditis<br>elegans, 439 aa.                  | 3.30E-54                  |    |
| 797 | cg43298242 | 143  | GATCTGTTGGC<br>AGGGCTCACAG<br>AGA[C/T]GGGG<br>TGAGGGGAGAG<br>ATCGTGGGT   | C | T | Val | Ile<br>(1170) | CONSERVATI<br>VE         | water_ch<br>annel         | Human Gene SWISSPROT-<br>ID:O14520 AQUAPORIN-7 LIKE<br>(AQUAPORIN ADIPOSE) (AQPAP) -<br>HOMO SAPIENS (HUMAN), 342 aa.   | 1.3E-163                  |    |
| 798 | cg43299610 | 842  | CTCCCAAGTGCC<br>CGCCCGACTAC<br>CAC[C/T]ACATC<br>CACACCGAGAT<br>CTCCCGGGA | C | T | His | Tyr<br>(1171) | NON-<br>CONSERVATI<br>VE | ATPase_<br>associat<br>ed | Human Gene Homologous to<br>SWISSPROT-ID:P39986 PROBABLE<br>CALCIUM-TRANSPORTING ATPASE<br>6 (EC 3.6.1.38) - SACCHAROMYCES<br>CEREVISIAE (BAKER'S YEAST),<br>1215 aa.                         | 1.40E-109                 |    |
| 799 | cg42532480 | 564  | TTTCCTGAATGA<br>ATGTTAAAGATT<br>C[T/A]GTCAAGG<br>TCAGTATGGCG<br>ATCCAAG  | T | A | Arg | End<br>(1172) | NON-<br>CONSERVATI<br>VE | cadherin                  | Human Gene Homologous to<br>SWISSPROT-ID:P79995 CADHERIN-<br>10 PRECURSOR - GALLUS GALLUS<br>(CHICKEN), 789 aa.[pcis:SPTREMBL-<br>ID:P79995 CADHERIN-10 - GALLUS<br>GALLUS (CHICKEN), 789 aa. | 6.00E-115                 |    |
| 800 | cg42926989 | 259  | GCAATGAGCTG<br>CTGGCAGCACCA<br>AAG[G/T]CTTATC<br>GCACCAGGAAA<br>GATGCAGC | G | T | Ala | Asp<br>(1173) | NON-<br>CONSERVATI<br>VE | cathepsi<br>n             | Human Gene Homologous to<br>SWISSPROT-ID:P08311<br>CATHEPSIN G PRECURSOR (EC<br>3.4.21.20) - HOMO SAPIENS<br>(HUMAN), 255 aa.   | 1.7E-136<br>(14q11.2<br>) | 14 |
| 801 | cg43991318 | 2521 | TGGTCCGGGAA<br>TACCTGGTGA<br>CCC[T/G]GCGGG<br>CCCGGCTGCCA<br>GGAGCTGCC   | T | G | Cys | Gly<br>(1174) | NON-<br>CONSERVATI<br>VE | collagen                  | Human Gene Similar to SWISSPROT-<br>ID:Q07092 COLLAGEN ALPHA<br>1(XVI) CHAIN PRECURSOR - HOMO<br>SAPIENS (HUMAN), 1603 aa.  | 1.3E-73<br>1 (1p34)       |    |

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|-----|------------|------|---|---|---|-----|---------------|--------------------------|------------|---|----------|-----------------|
| 802 | cg43920512 | 1467 | AATCAAAGTAT<br>CATGGTGTCT<br>CT/CJCCCTCAAC<br>CCACCAGAGAC<br>ACTAAAT    | T | C | Leu | Pro<br>(1175) | NON-<br>CONSERVATI<br>VE | cyclin     | Human Gene SWISSPROT-<br>ID:P20248 G2/MITOTIC-SPECIFIC<br>CYCLIN A - HOMO SAPIENS<br>(HUMAN), 432 aa.   | 4.1E-231 | 4 (4q27)        |
| 803 | cg43063374 | 1763 | AGAGATTGAAC<br>GTGTGGTTGGC<br>AGA[A/C]ACCGG<br>AGCCCCTGCT<br>GCAGGACAG  | A | C | Asn | His<br>(1176) | NON-<br>CONSERVATI<br>VE | cyto450    | Human Gene SWISSNEW-ID:P33259<br>CYTOCHROME P450 2C17 (EC<br>1.14.14.1) (CYPIIC17) (P450-254C) -<br>HOMO SAPIENS (HUMAN), 468<br>aa.   pcls:SWISSPROT-ID:P33259<br>CYTOCHROME P450 IIC17 (EC<br>1.14.14.1) (P450-254C) - HOMO<br>SAPIENS (HUMAN), 468 aa. | 3.2E-254 | 10<br>(10q24.1) |
| 804 | cg21416244 | 360  | GGGTGAACGT<br>CTATCCACCATT<br>ATC/TJATCTATT<br>CAGGCACATTC<br>AGGACCT   | C | T | Ser | Leu<br>(1177) | NON-<br>CONSERVATI<br>VE | cytochrome | Human Gene Similar to SWISSPROT-<br>ID:P98001 CYTOCHROME C<br>OXIDASE POLYPEPTIDE I (EC<br>1.9.3.1) - SACCHAROMYCES<br>DOUGLASII (YEAST), 534 aa.   | 5.5E-69  |                 |
| 805 | cg44017721 | 217  | AGATAGGAGTT<br>GAAGGTGCAGA<br>GG[C/T]CACGC<br>TGGGCAGCGCC<br>AGCACGAAG  | C | T | Ala | Thr<br>(1178) | NON-<br>CONSERVATI<br>VE | cytochrome | Human Gene Similar to SPTREMBL-<br>ID:O00761 CYTOCHROME<br>OXIDASE SUBUNIT VIA HEART<br>ISOFORM PRECURSOR (EC 1.9.3.1)<br>(CYTOCHROME-C OXIDASE)<br>(CYTOCHROME A(3))<br>(CYTOCHROME AA(3)) - HOMO<br>SAPIENS (HUMAN), 97 aa.                             | 2.4E-52  | 22              |
| 806 | cg43275625 | 1105 | TGGTACTCCTTT<br>GCCGCCAGCTT<br>GGJ/A/GJCTCATG<br>GTACACGTTGG<br>GTTTGGA | A | G | Ser | Pro<br>(1179) | NON-<br>CONSERVATI<br>VE | deaminase  | Human Gene SPTREMBL-ID:O00465<br>DSRNA ADENOSINE DEAMINASE<br>DRADA2C - HOMO SAPIENS<br>(HUMAN), 714 aa.  | 0        | 21              |



|     |            |      |   |   |   |     |               |                      |               |  |   |    |
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| 807 | cg43312829 | 1402 | TAGTGAATACT<br>CCAATCAAAGAC<br>A[A/G]CAGGACT<br>CCATGTAACTGA<br>ATATGA  | A | G | Thr | Ala<br>(1180) | NON-<br>CONSERVATIVE | dehydrogenase | Human Gene SWISSPROT-<br>ID:Q16134 ELECTRON TRANSFER<br>FLAVOPROTEIN-UBIQUINONE<br>OXIDOREDUCTASE PRECURSOR<br>(EC 1.5.5.1) (ETF-QO) (ETF-<br>UBIQUINONE OXIDOREDUCTASE)<br>(ETF DEHYDROGENASE)<br>(ELECTRON-TRANSFERRING-<br>FLAVOPROTEIN<br>DEHYDROGENASE) - HOMO<br>SAPIENS (HUMAN), 617 aa.  | 0 | 4  |
| 808 | cg43959136 | 1144 | TGGGCCAACAA<br>GCTTGAGTGCG<br>ATC[C/T]GGTCT<br>GCAATGATGGA<br>GGAATTGCC | C | T | Arg | Gln<br>(1181) | NON-<br>CONSERVATIVE | dehydrogenase | Human Gene SWISSPROT-ID:P11586<br>C-1-TETRAHYDROFOLATE<br>SYNTHASE, CYTOPLASMIC (C1-<br>THF SYNTHASE)<br>(METHYLENETETRAHYDROFOLAT<br>E DEHYDROGENASE (EC 1.5.1.5) /<br>METHENYL TETRAHYDROFOLATE<br>CYCLOHYDROLASE (EC 3.5.4.9) /<br>FORMYL TETRAHYDROFOLATE<br>SYNTHETASE (EC 6.3.4.3)) - HOMO<br>SAPIENS (HUMAN), 934<br>aa.   pcds:SWISSPROT-ID:P11586 C-1-<br>TETRAHYDROFOLATE SYNTHASE,<br>CYTOPLASMIC<br>(METHYLENETETRAHYDROFOLAT<br>E DEHYDROGENASE (EC 1.5.1.5) /<br>METHENYL TETRAHYDROFOLATE<br>CYCLOHYDROLASE (EC 3.5.4.9) /<br>FORMYL TETRAHYDROFOLATE<br>SYNTHETASE (EC 6.3.4.3)) (C1-THF<br>SYNTHASE) - HOMO SAPIENS<br>(HUMAN), 934 aa. | 0 | 14 |



|     |            |      |   |   |   |     |               |                          |                  |  |           |    |
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| 815 | cg39709402 | 57   | GATGCTGGAGG<br>ACTTCAAGAAAG<br>AC[A/G]TGAAGA<br>ACTCCCTTAGAG<br>AAACACA   | A | G | Met | Val<br>(1188) | NON-<br>CONSERVATI<br>VE | dna_rna<br>_bind | Human Gene Similar to SPTREMBL-<br>ID:O08872 PUTATIVE RNA BINDING<br>PROTEIN 1 - RATTUS<br>NORVEGICUS (RAT), 362 aa<br>(fragment).                         | 3.20E-57  |    |
| 816 | cg39709402 | 76   | AAAGACATGAA<br>GAACTCCCTTAG<br>AG[A/G]AACACA<br>GGAACACATTAA<br>TAAACAA   | A | G | Glu | Gly<br>(1189) | NON-<br>CONSERVATI<br>VE | dna_rna<br>_bind | Human Gene Similar to SPTREMBL-<br>ID:O08872 PUTATIVE RNA BINDING<br>PROTEIN 1 - RATTUS<br>NORVEGICUS (RAT), 362 aa<br>(fragment).                         | 3.20E-57  |    |
| 817 | cg39709402 | 94   | CTTAGAGAAACA<br>CAGGAAAAACATT<br>A[A/G]TAAACAA<br>GTAGAAAGCCTA<br>CAGAGAG | A | G | Asn | Ser<br>(1190) | NON-<br>CONSERVATI<br>VE | dna_rna<br>_bind | Human Gene Similar to SPTREMBL-<br>ID:O08872 PUTATIVE RNA BINDING<br>PROTEIN 1 - RATTUS<br>NORVEGICUS (RAT), 362 aa<br>(fragment).                         | 3.20E-57  |    |
| 818 | cg39709402 | 96   | TAGAGAAACACA<br>GGAAACATTAA<br>T[A/G]AACAAAGT<br>AGAAGCCTACA<br>GAGAGGA   | A | G | Lys | Glu<br>(1191) | NON-<br>CONSERVATI<br>VE | dna_rna<br>_bind | Human Gene Similar to SPTREMBL-<br>ID:O08872 PUTATIVE RNA BINDING<br>PROTEIN 1 - RATTUS<br>NORVEGICUS (RAT), 362 aa<br>(fragment).                         | 3.20E-57  | 16 |
| 819 | cg43950268 | 1949 | TTTGCTATGTCC<br>TCCTTGACCTCC<br>T[G/A]CTCGGTG<br>GCGGTCACAAT<br>GCCCTCC   | G | A | Gln | End<br>(1192) | NON-<br>CONSERVATI<br>VE | eph              | Human Gene TREMBLNEW-<br>ID:G2865466 HEAT SHOCK<br>PROTEIN 75 - HOMO SAPIENS<br>(HUMAN), 649 aa.   | 0.00E+00  |    |
| 820 | cg43985169 | 540  | AAGACGAATGG<br>GTGGTGGTAGA<br>GATT[C]CTGAA<br>GAAATGGAATA<br>GATGGTGA     | T | C | Ser | Pro<br>(1193) | NON-<br>CONSERVATI<br>VE | eph              | Human Gene Homologous to<br>SWISSPROT-ID:P25685 DNAJ<br>PROTEIN HOMOLOG 1 (HDJ-1)<br>(HEAT SHOCK PROTEIN 40)<br>(HSP40) - HOMO SAPIENS<br>(HUMAN), 340 aa. | 2.40E-123 |    |
| 821 | cg43997616 | 2250 | AAAGCCAGCGG<br>AGCCGTAAGCA<br>TCAIT/CJACTGCT<br>TCCTCTTCACCT<br>CATCACT   | T | C | Tyr | Cys<br>(1194) | NON-<br>CONSERVATI<br>VE | eph              | Human Gene Similar to<br>TREMBLNEW-ID:G2735762 HEAT<br>SHOCK PROTEIN DNAJ -<br>LEPTOSPIRA INTERROGANS, 369<br>aa.  | 1.40E-55  |    |

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|-----|------------|------|---|---|---|-----|---------------|----------------------|--------------|--|-----------|---------------|
| 822 | cg43319420 | 992  | CACGACAACTA<br>CAGAAACAACC<br>CCTT/CJCCACA<br>ACTCCGGCAC<br>TGCTTCTGC   | T | C | Phe | Ser<br>(1195) | NON-<br>CONSERVATIVE | esterase     | Human Gene Similar to SWISSPROT-ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa.   pcds:SWISSPROT-ID:Q23917 3',5'-CYCLIC-NUCLEOTIDE PHOSPHODIESTERASE REGA (EC 3.1.4.17) (PDEASE REGA) - DICTYOSTELIUM DISCOIDEUM (SLIME MOLD), 793 aa. | 3.30E-60  | 21            |
| 823 | cg44034764 | 382  | GAGGTCCAGGC<br>TGGGCAGGACA<br>GTC/T/CJCCCCA<br>TGGTGCCGTA<br>CAGCCTCTT  | T | C | Glu | Gly<br>(1196) | NON-<br>CONSERVATIVE | glycoprotein | Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.   | 0.00E+00  | 7<br>(Xp21.2) |
| 824 | cg43991224 | 217  | TCTCATCTGTCT<br>ACCTACAGCCT<br>GGT/AJTTGGGT<br>CATGGCAGCAG<br>TGGTGCTG  | T | A | Val | Asp<br>(1197) | NON-<br>CONSERVATIVE | glycoprotein | Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa (fragment).   | 1.50E-139 |               |
| 825 | cg44018623 | 1824 | TACCATCTCTGT<br>TTTTACCACTGG<br>T[G/A]GCTCTGA<br>ACAACAAATAAT<br>TTGTGG | G | A | Pro | Leu<br>(1198) | NON-<br>CONSERVATIVE | glycoprotein | Human Gene Homologous to SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.   | 1.90E-114 | 6             |
| 826 | cg38924741 | 598  | AAAGAGGAGAA<br>TGGTGACTTTGC<br>CTT/CJATTCAGA<br>GTGGAACGAGC<br>TGAAAGG  | T | C | Leu | Ser<br>(1199) | NON-<br>CONSERVATIVE | glycoprotein | Human Gene Similar to SWISSPROT-ID:P04196 HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-PROLINE RICH GLYCOPROTEIN) (HPRG) - HOMO SAPIENS (HUMAN), 525 aa.   | 3.30E-55  |               |

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| 827 | cg43322513 | 13082 | TTCCTGTTCTTC<br>ACATGGTGAGC<br>CC[C/T]GCCCTG<br>CTGTCTGCTTGC<br>ATTCGGG | C | T | Arg | Gln<br>(1200) | NON-<br>CONSERVATIVE | glycoprotein | Human Gene Similar to SWISSPROT-<br>ID:P13983 EXTENSIN PRECURSOR<br>(CELL WALL HYDROXYPROLINE-<br>RICH GLYCOPROTEIN) -<br>NICOTIANA TABACUM (COMMON<br>TOBACCO), 620 aa.   | 3.30E-54 | 12 |
| 828 | cg44913214 | 2306  | GAACACAAACAA<br>GAAAAAACAGA<br>GT[C/T]TGGGAC<br>TCATCCAAAAGG<br>GACGAGA | C | T | Ser | Phe<br>(1201) | NON-<br>CONSERVATIVE | helicase     | Human Gene TREMBLNEW-<br>ID:G2801555 PUTATIVE ATP-<br>DEPENDENT MITOCHONDRIAL<br>RNA HELICASE - HOMO SAPIENS<br>(HUMAN), 786 aa.   | 0.00E+00 | 10 |
| 829 | cg39529972 | 278   | TGGCCTCGAC<br>ATCATCCCTGA<br>CG[A/G]GGACTT<br>AAAGGGTAGCA<br>ATTCGTAT   | A | G | Ser | Pro<br>(1202) | NON-<br>CONSERVATIVE | hydrolase    | Human Gene Similar to SWISSPROT-<br>ID:Q01477 UBIQUITIN CARBOXYL-<br>TERMINAL HYDROLASE 3 (EC<br>3.1.2.15) (UBIQUITIN-<br>THIOLESTERASE 3) (UBIQUITIN-<br>SPECIFIC PROCESSING<br>PROTEASE 3) (DEUBIQUITINATING<br>ENZYME 3) - SACCCHAROMYCES<br>CEREVISIAE (BAKER'S YEAST), 912<br>aa.   | 1.00E-52 |    |
| 830 | cg43925670 | 2309  | TAGTTTGCCCAA<br>ACCAGCATCAC<br>CT[C/G]GGAAC<br>TTTCTTCCATCA<br>AGTCAGC  | C | G | Arg | Pro<br>(1203) | NON-<br>CONSERVATIVE | interferon   | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.<br>ipclis:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0.00E+00 | 1  |

|     |            |      |  |   |   |     |               |                      |            |  |          |   |
|-----|------------|------|--|---|---|-----|---------------|----------------------|------------|--|----------|---|
| 831 | cg43925670 | 2369 | TTTGTCACTC<br>TTCTCTCATTT<br>T/A/G/AATTAAAGT<br>TTTAAATCGTTG<br>CTCAG    | A | G | Leu | Ser<br>(1204) | NON-<br>CONSERVATIVE | interferon | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.pcls:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0.00E+00 | 1 |
| 832 | cg43925670 | 2458 | CCTCTAATCCTT<br>TTAGTAGAACAA<br>T[G/T]TTCCTGTA<br>TTTTTTTCCCAT<br>CTTTA  | G | T | Asn | Lys<br>(1205) | NON-<br>CONSERVATIVE | interferon | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.pcls:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0.00E+00 | 1 |
| 833 | cg43925670 | 2467 | CTTTTAGTAGAA<br>CAATGTTCTTGT<br>A[T/G]TTTTTTTCC<br>CATCTTTACAGA<br>CATAA | T | G | Lys | Asn<br>(1206) | NON-<br>CONSERVATIVE | interferon | Human Gene SWISSPROT-<br>ID:Q16666 GAMMA-INTERFERON-<br>INDUCIBLE PROTEIN IFI-16<br>(INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR) -<br>HOMO SAPIENS (HUMAN), 729<br>aa.pcls:SPTREMBL-ID:Q16666<br>IFI16=INTERFERON-INDUCIBLE<br>MYELOID DIFFERENTIATION<br>TRANSCRIPTIONAL ACTIVATOR -<br>HOMO SAPIENS (HUMAN), 729 aa<br>(fragment). | 0.00E+00 | 1 |

|     |            |      |   |   |   |     |               |                          |           |  |           |          |
|-----|------------|------|---|---|---|-----|---------------|--------------------------|-----------|--|-----------|----------|
| 834 | cg43331742 | 845  | TCCTCGAGGTG<br>CTTCCACAGA<br>CTC[G/A]ATTTCT<br>GAGTTTCCACA<br>GAAAAGA   | G | A | Ser | Leu<br>(1207) | NON-<br>CONSERVATI<br>VE | isomerase | Human Gene Homologous to<br>SWISSPROT-ID:P70473 2-<br>ARYLPROPYONYL-COA EPIMERASE<br>(EC 5.-.-) - RATTUS NORVEGICUS<br>(RAT), 361 aa.  | 5.60E-131 |          |
| 835 | cg43253796 | 1812 | GAAATGGATCTT<br>ATTGGACTTTG<br>C[G/T]ACAAGAC<br>TGCCGAGAGAT<br>TTTCCCA  | G | T | Arg | Leu<br>(1208) | NON-<br>CONSERVATI<br>VE | kinase    | Human Gene SWISSNEW-ID:P42338<br>PHOSPHATIDYLINOSITOL 3-<br>KINASE CATALYTIC SUBUNIT,<br>BETA ISOFORM (EC 2.7.1.137) (PI3-<br>KINASE P110 SUBUNIT BETA)<br>(PTDINS-3-KINASE P110) (PI3K) -<br>HOMO SAPIENS (HUMAN), 1070<br>aa. pds:SWISSPROT-ID:P42338<br>PHOSPHATIDYLINOSITOL 3-<br>KINASE CATALYTIC SUBUNIT,<br>BETA ISOFORM (EC 2.7.1.137) (PI3-<br>KINASE P110 SUBUNIT BETA)<br>(PTDINS-3-KINASE P110) (PI3K) -<br>HOMO SAPIENS (HUMAN), 1070 aa. | 0.00E+00  |          |
| 836 | cg43257400 | 2094 | GACATCAGCAT<br>GGCTGCCCCCG<br>ACTT[C]CAGCA<br>GAACATGATCAT<br>TCTCTGAC  | T | C | Ser | Pro<br>(1209) | NON-<br>CONSERVATI<br>VE | kinase    | Human Gene SPTREMBL-ID:Q60680<br>CONSERVED HELIX-LOOP-HELIX<br>UBIQUITOUS KINASE - MUS<br>MUSCULUS (MOUSE), 745 aa.  | 0.00E+00  | 10       |
| 837 | cg43974480 | 686  | TCACGGACTTTG<br>GACTGTCCAAA<br>T[G/T]GGCCTCA<br>TGAGCCTGACA<br>ACGAACT  | G | T | Met | Ile<br>(1210) | NON-<br>CONSERVATI<br>VE | kinase    | Human Gene SPTREMBL-ID:O00114<br>HYPOTHETICAL HUMAN SERINE-<br>THREONINE PROTEIN KINASE<br>R31240_1 - HOMO SAPIENS<br>(HUMAN), 1237 aa (fragment).   | 0.00E+00  |          |
| 838 | cg43922705 | 4337 | CAAACCGGCTTT<br>CTCCATGGTGC<br>CC[T/C]GCCAAA<br>CCCTGGAGTTC<br>CCAGGCTG | T | C | Gln | Arg<br>(1211) | NON-<br>CONSERVATI<br>VE | kinase    | Human Gene SWISSPROT-<br>ID:P27987 1D-MYO-INOSITOL-<br>TRISPHOSPHATE 3-KINASE B (EC<br>2.7.1.127) (INOSITOL 1,4,5-<br>TRISPHOSPHATE 3-KINASE) (IP3K)<br>(IP3 3-KINASE) - HOMO SAPIENS<br>(HUMAN), 505 aa (fragment).   | 3.80E-279 | 1 (1q41) |

|     |            |      |   |   |   |     |               |                          |                    |   |           |    |
|-----|------------|------|---|---|---|-----|---------------|--------------------------|--------------------|---|-----------|----|
| 839 | cg38438124 | 1460 | TGCAAAAACTGT<br>TAAACATGGCG<br>CTG/C/GCGCGG<br>AGATCTCCACC<br>GTGAACCC  | G | C | Gly | Arg<br>(1212) | NON-<br>CONSERVATI<br>VE | kinase             | Human Gene SWISSNEW-ID:O70172<br>PHOSPHATIDYLINOSITOL-4-<br>PHOSPHATE 5-KINASE TYPE II<br>ALPHA (EC 2.7.1.68) (PIP5KII-<br>ALPHA) (1-<br>PHOSPHATIDYLINOSITOL-4-<br>PHOSPHATE KINASE) (PTDINS(4)P-<br>5-KINASE B ISOFORM)<br>(DIPHOSPHOINOSITIDE KINASE) -<br>MUS MUSCULUS (MOUSE), 405 aa. | 2.80E-216 | 10 |
| 840 | cg42703622 | 385  | GTATGCAGCAA<br>CAAGAGCAACT<br>CTG/A/GJAGAAG<br>GAATTTGGAGG<br>TGGCCACAT | A | G | Lys | Glu<br>(1213) | NON-<br>CONSERVATI<br>VE | kinase             | Human Gene SPTREMBL-ID:Q12792<br>PROTEIN TYROSINE KINASE -<br>HOMO SAPIENS (HUMAN), 350 aa.   | 3.00E-187 | 12 |
| 841 | cg42703622 | 395  | ACAAGAGCAAC<br>TCTGAAGAAGG<br>AAT/T/CJTGAG<br>GTGCCACATT<br>AAAGATGAA   | T | C | Phe | Ser<br>(1214) | NON-<br>CONSERVATI<br>VE | kinase             | Human Gene SPTREMBL-ID:Q12792<br>PROTEIN TYROSINE KINASE -<br>HOMO SAPIENS (HUMAN), 350 aa.   | 3.00E-187 | 12 |
| 842 | cg41501665 | 96   | GAGTACACCAT<br>CAAGTCGCACT<br>CCA/G/AJCTTGC<br>CGCCCAACAAC<br>AGCTACGCC | G | A | Ser | Asn<br>(1215) | NON-<br>CONSERVATI<br>VE | kinase             | Human Gene Similar to<br>TREMBLNEW-ID:D1025880 ZIP-<br>KINASE - HOMO SAPIENS<br>(HUMAN), 454 aa.  | 2.70E-76  |    |
| 843 | cg25143358 | 457  | GCTTTATGGTA<br>TCGACATCCAAT<br>G/C/TJGTCGATG<br>TCCTCCACAACC<br>TCCACG  | C | T | Ala | Thr<br>(1216) | NON-<br>CONSERVATI<br>VE | kinase             | Human Gene Similar to SWISSPROT-<br>ID:P46546 GLUTAMATE 5-KINASE<br>(EC 2.7.2.11) (GAMMA-GLUTAMYL<br>KINASE) (GK) -<br>CORYNEBACTERIUM<br>GLUTAMICUM, 369 aa.   | 2.70E-51  |    |
| 844 | cg29023997 | 179  | TGCATGGTTTCC<br>ATTTCATCTG<br>G/A/GJTGCGATG<br>GAGCACCATGT<br>GCGCACC   | A | G | Asp | Gly<br>(1217) | NON-<br>CONSERVATI<br>VE | kinasere<br>ceptor | Human Gene SWISSPROT-<br>ID:P36896 SERINE/THREONINE-<br>PROTEIN KINASE RECEPTOR R2<br>PRECURSOR (EC 2.7.1.37) (SKR2)<br>(ACTIVIN RECEPTOR-LIKE KINASE<br>4) (ALK-4) (ACTR-IB) - HOMO<br>SAPIENS (HUMAN), 505 aa.  | 9.30E-280 | 12 |



|     |            |      |   |   |   |     |               |                          |                  |  |           |    |
|-----|------------|------|---|---|---|-----|---------------|--------------------------|------------------|--|-----------|----|
| 845 | cg43975720 | 3917 | CATCCACCCAG<br>CCCAAGATGAC<br>CGG[A/C]CCTTT<br>TACCAATTTGAG<br>GCTGCGTG   | A | C | Thr | Pro<br>(1218) | NON-<br>CONSERVATI<br>VE | kinesin          | Human Gene SWISSPROT-<br>ID:Q12756 KINESIN-LIKE PROTEIN<br>KIF1A (AXONAL TRANSPORTER OF<br>SYNAPTIC VESICLES) - HOMO<br>SAPIENS (HUMAN), 1690 aa.  | 0.00E+00  | 2  |
| 846 | cg44013875 | 1710 | GCCATGGAGAG<br>GCTGCAGGAGA<br>CAG[A/G]GAAGA<br>TTATAGCTGAGC<br>TGAACGAG   | A | G | Glu | Gly<br>(1219) | NON-<br>CONSERVATI<br>VE | kinesin          | Human Gene SWISSNEW-ID:Q43896<br>KINESIN-LIKE PROTEIN KIF1C -<br>HOMO SAPIENS (HUMAN), 1103<br>aa.   pcds:TREMBLNEW-ID:G2738149<br>KINESIN-LIKE MOTOR PROTEIN<br>KIF1C - HOMO SAPIENS (HUMAN),<br>1103 aa. | 0.00E+00  |    |
| 847 | cg44009224 | 2806 | TTTGGATCCTGA<br>AAATGTTGTATT<br>TTT[C/G]ATGTTGGA<br>GGTTACCCACC<br>TGATTT | T | C | Tyr | His<br>(1220) | NON-<br>CONSERVATI<br>VE | laminin          | Human Gene SWISSPROT-<br>ID:Q16787 LAMININ ALPHA-3 CHAIN<br>PRECURSOR (EPILGRIN 170 KD<br>SUBUNIT) (E170) - HOMO SAPIENS<br>(HUMAN), 1713 aa.  | 0.00E+00  |    |
| 848 | cg42930646 | 1228 | TGATGCGGATA<br>GCGTATGGATG<br>GAA[A/G]TGGAC<br>GATGAGGAGGA<br>CCTGCCTTC   | A | G | Met | Val<br>(1221) | NON-<br>CONSERVATI<br>VE | laminin          | Human Gene SWISSPROT-<br>ID:P07221 CALSEQUESTIN,<br>SKELETAL MUSCLE ISOFORM<br>PRECURSOR (ASPARTACTIN)<br>(LAMININ-BINDING PROTEIN) -<br>ORYCTOLAGUS CUNICULUS<br>(RABBIT), 395 aa.                        | 1.80E-198 | 1  |
| 849 | cg43935885 | 3745 | CCAGACAGCAC<br>CACTGGAACCC<br>CTC[C/T]TAGCA<br>GCGCACCCAGAC<br>CCGAAGAAC  | C | T | Pro | Leu<br>(1222) | NON-<br>CONSERVATI<br>VE | MHC              | Human Gene SPTREMBL-ID:P79457<br>MALE-SPECIFIC<br>HISTOCOMPATIBILITY ANTIGEN H-<br>YDB - MUS MUSCULUS (MOUSE),<br>1186 aa.   | 7.20E-173 |    |
| 850 | cg42928872 | 1807 | GAGCTGCAGAG<br>GAGGCTGGACC<br>AGT[C/T]CATTG<br>GGAAGCCCTCA<br>CTGTTCATC   | C | T | Ser | Phe<br>(1223) | NON-<br>CONSERVATI<br>VE | misc_ch<br>annel | Human Gene TREMBLNEW-<br>ID:G2465531 KIDNEY AND<br>CARDIAC VOLTAGE DEPENDENT<br>K+ CHANNEL - HOMO SAPIENS<br>(HUMAN), 676 aa.  | 0.00E+00  | 11 |

|     |            |      |  |   |   |     |               |                          |                  |   |          |                 |
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| 851 | cg44019843 | 929  | GAGTGACCCGC<br>CTCCCTGGTCC<br>AAGATATGTG<br>GAGTACACCTTC<br>ACAGGGAT   | A | T | Asn | Tyr<br>(1224) | NON-<br>CONSERVATI<br>VE | misc_ch<br>annel | Human Gene SPTREMBL-ID:Q15478<br>SODIUM CHANNEL ALPHA<br>SUBUNIT - HOMO SAPIENS<br>(HUMAN), 1836 aa.  | 0.00E+00 | 17<br>(17q23.1) |
| 852 | cg44128805 | 1396 | AGTGCACACAG<br>TGAGCTCAGAG<br>CTT[C/T]CCCC<br>GAAACCGAAA<br>GTTTCAACT  | C | T | Glu | Lys<br>(1225) | NON-<br>CONSERVATI<br>VE | nuclease         | Human Gene Similar to SWISSPROT-<br>ID:P54278 PMS1 PROTEIN<br>HOMOLOG 2 (DNA MISMATCH<br>REPAIR PROTEIN PMS2) - HOMO<br>SAPIENS (HUMAN), 862 aa.  | 1.60E-76 | 7               |
| 853 | cg38642684 | 304  | TTTCTGATAATC<br>ATTTAAGGTATG<br>T[AT]AGTTGCTA<br>GTATTTAATTTA<br>ACCTT | A | T | Leu | End<br>(1226) | NON-<br>CONSERVATI<br>VE | nuclease         | Human Gene Similar to SWISSNEW-<br>ID:P10266 RETROVIRUS-RELATED<br>POL POLYPROTEIN [CONTAINS:<br>REVERSE TRANSCRIPTASE (EC<br>2.7.7.49); ENDONUCLEASE] -<br>HOMO SAPIENS (HUMAN), 874<br>aa.   pcis:SWISSPROT-ID:P10266<br>RETROVIRUS-RELATED POL<br>POLYPROTEIN (REVERSE<br>TRANSCRIPTASE (EC 2.7.7.49);<br>ENDONUCLEASE) - HOMO<br>SAPIENS (HUMAN), 874 aa. | 2.60E-50 |                 |
| 854 | cg38642684 | 417  | CTTTTCAGGTG<br>CAATGATTAAAC<br>C[AT]CTTAACTG<br>TGCATTCCTTAT<br>GACAG  | A | T | Ser | Arg<br>(1227) | NON-<br>CONSERVATI<br>VE | nuclease         | Human Gene Similar to SWISSNEW-<br>ID:P10266 RETROVIRUS-RELATED<br>POL POLYPROTEIN [CONTAINS:<br>REVERSE TRANSCRIPTASE (EC<br>2.7.7.49); ENDONUCLEASE] -<br>HOMO SAPIENS (HUMAN), 874<br>aa.   pcis:SWISSPROT-ID:P10266<br>RETROVIRUS-RELATED POL<br>POLYPROTEIN (REVERSE<br>TRANSCRIPTASE (EC 2.7.7.49);<br>ENDONUCLEASE) - HOMO<br>SAPIENS (HUMAN), 874 aa. | 2.60E-50 |                 |

|     |            |      |  |   |     |               |                          |             |  |           |                 |
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| 855 | cg44913844 | 1194 | CCAGTTGGTAAA<br>CTGGTCTTAAAC<br>C[G/A]GAATCCA<br>GTTAATTACTTT<br>GCTGAG  | A | Arg | Gln<br>(1228) | NON-<br>CONSERVATI<br>VE | peroxidase  | Human Gene SWISSPROT-<br>ID:P04040 CATALASE (EC 1.11.1.6) -<br>HOMO SAPIENS (HUMAN), 527 aa.   | 2.70E-296 | 11<br>(11p13)   |
| 856 | cg40084915 | 5005 | TCTGCGGTCTG<br>GGGAGATGAGG<br>GCC[T/C]CAAAC<br>AGCACCTGATAT<br>TCATTGGG  | C | Glu | Gly<br>(1229) | NON-<br>CONSERVATI<br>VE | phosphatase | Human Gene SPTREMBL-ID:O00197<br>RECEPTOR PROTEIN TYROSINE<br>PHOSPHATASE HPTP-J<br>PRECURSOR - HOMO SAPIENS<br>(HUMAN), 1436 aa.  | 0.00E+00  | 1               |
| 857 | cg42720088 | 214  | AAAGCTCAGAG<br>AGATCTGGGCT<br>ATG[A/T]GCCAC<br>TTGTCAGCTGG<br>GAGGAAGCC  | T | Glu | Val<br>(1230) | NON-<br>CONSERVATI<br>VE | reductase   | Human Gene Similar to SWISSPROT-<br>ID:P22072 3 BETA-<br>HYDROXYSTEROID<br>DEHYDROGENASE/DELTA 5->4-<br>ISOMERASE TYPE II (3BETA-HSD<br>II) (3-BETA-HYDROXY-DELTA(5)-<br>STEROID DEHYDROGENASE (EC<br>1.1.1.145) (3-BETA-HYDROXY-5-<br>ENE STEROID DEHYDROGENASE)<br>(PROGESTERONE REDUCTASE) /<br>STEROID DELTA-ISOMERASE (EC<br>5.3.3.1) (DELTA-5-3-KETOSTEROID<br>ISOMERASE)) - RATTUS<br>NORVEGICUS (RAT), 372 aa. | 2.40E-50  |                 |
| 858 | cg43957486 | 1528 | CGCTCCTGCAC<br>CGCATCCGCGA<br>CGC[A/T]GTCCT<br>GCAACGACCTC<br>TGCGAGCAC  | T | Gln | Leu<br>(1231) | NON-<br>CONSERVATI<br>VE | struct      | Human Gene SWISSPROT-<br>ID:P07204 THROMBOMODULIN<br>PRECURSOR (FETOMODULIN) (TM)<br>(CD141 ANTIGEN) - HOMO<br>SAPIENS (HUMAN), 575 aa.  | 0.00E+00  | 20<br>(20p11.2) |
| 859 | cg40148056 | 1462 | CTCAGAGACCC<br>CTAACAAACCCA<br>GCA[G/C]CCACA<br>GAGCGGAACAC<br>TTAAGGATC | C | Gln | His<br>(1232) | NON-<br>CONSERVATI<br>VE | struct      | Human Gene SPTREMBL-ID:Q92777<br>SYNAPSIN IIB - HOMO SAPIENS<br>(HUMAN), 478 aa.   | 2.90E-260 | 3 (3p)          |

|     |            |     |  |   |   |     |               |                          |                      |  |           |    |
|-----|------------|-----|--|---|---|-----|---------------|--------------------------|----------------------|--|-----------|----|
| 860 | cg43981852 | 473 | CACCTCCTCCA<br>GCTTCCAGCC<br>TCC[C]CGGCT<br>CTGGCCAGGCT<br>GCCGCTGGG     | C | T | Gly | Glu<br>(1233) | NON-<br>CONSERVATI<br>VE | struct               | Human Gene Homologous to<br>SWISSPROT-ID:Q92176 CORONIN-<br>LIKE PROTEIN P57 - BOS TAURUS<br>(BOVINE), 461 aa.   | 7.80E-113 |    |
| 861 | cg42522566 | 318 | GCAGCCAAAGAT<br>CATCAAAGTGAA<br>GA/GJCGTAAA<br>GGACCGGGAGG<br>ATGTGAAG   | A | G | Asn | Ser<br>(1234) | NON-<br>CONSERVATI<br>VE | struct               | Human Gene Similar to SWISSPROT-<br>ID:P07313 MYOSIN LIGHT CHAIN<br>KINASE, SKELETAL MUSCLE (EC<br>2.7.1.117) (MLCK) - ORYCTOLAGUS<br>CUNICULUS (RABBIT), 607 aa.  | 6.00E-55  |    |
| 862 | cg43297806 | 966 | ATAGTAGCCAG<br>GGACAAAGACAG<br>CGG[T/C]TCTGC<br>AGGGAGCGTAG<br>TGCCAGAGG | T | C | Asn | Ser<br>(1235) | NON-<br>CONSERVATI<br>VE | sulfotran<br>sferase | Human Gene SWISSPROT-<br>ID:P52849 HEPARIN SULFATE N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE (EC 2.8.2.-)<br>(N- HSST) (N-HEPARIN SULFATE<br>SULFOTRANSFERASE)<br>(GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE) - HOMO<br>SAPIENS (HUMAN), 883<br>aa.pcls:TREMBLNEW-ID:G2792518<br>HEPARAN GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE-2 - HOMO<br>SAPIENS (HUMAN), 883 aa. | 0.00E+00  | 10 |

|     |            |      |   |   |   |     |               |                          |                      |   |                            |                |
|-----|------------|------|---|---|---|-----|---------------|--------------------------|----------------------|---|----------------------------|----------------|
| 863 | cg43297806 | 994  | TGCAGGGAGCG<br>TAGTGCCAGAG<br>GGG[T/C]CTGGG<br>AGGAGGCTGAA<br>ATCACCTGA | T | C | Thr | Ala<br>(1236) | NON-<br>CONSERVATI<br>VE | sulfotran<br>sferase | Human Gene SWISSPROT-<br>ID:P52849 HEPARIN SULFATE N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE (EC 2.8.2.-)<br>(N- HSSST) (N-HEPARIN SULFATE<br>SULFOTRANSFERASE)<br>(GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE) - HOMO<br>SAPIENS (HUMAN), 883<br>aa.jpcls:TREMBLNEW-ID:G2792518<br>HEPARAN GLUCOSAMINYL N-<br>DEACETYLASE/N-<br>SULFOTRANSFERASE-2 - HOMO<br>SAPIENS (HUMAN), 883.aa | 0.00E+00                   | 10             |
| 864 | cg43987111 | 1337 | AGTAGTCTGCG<br>TCTCCATAGAGT<br>TT[C/A]CTCATGA<br>CTGAGTTCCTGG<br>TCTGGA | C | A | Arg | Ser<br>(1237) | NON-<br>CONSERVATI<br>VE | synthase             | Human Gene SWISSPROT-<br>ID:P17812 CTP SYNTHASE (EC<br>6.3.4.2) (UTP--AMMONIA LIGASE)<br>(CTP SYNTHETASE) - HOMO<br>SAPIENS (HUMAN), 591 aa.  | 0.00E+00                   | 18<br>(1p34.1) |
| 865 | cg43976335 | 633  | GAAATGCACTG<br>GACCACTCGGG<br>CAG[G/A]GCTGC<br>CAGGCCGTAGC<br>AGGCAATTC | G | A | Pro | Ser<br>(1238) | NON-<br>CONSERVATI<br>VE | synthase             | Human Gene SWISSPROT-<br>ID:P48637 GLUTATHIONE<br>SYNTHETASE (EC 6.3.2.3)<br>(GLUTATHIONE SYNTHASE) (GSH<br>SYNTHETASE) (GSH-S) - HOMO<br>SAPIENS (HUMAN), 474 aa.  | 5.30E-240<br>(20q11.2<br>) | 20             |
| 866 | cg39515668 | 605  | ACGCACGAACC<br>GGTCATACTGG<br>TCG[G/T]TGATC<br>CAGGAACGGTC<br>GCACAGCTG | G | T | Thr | Asn<br>(1239) | NON-<br>CONSERVATI<br>VE | synthase             | Human Gene Similar to SWISSNEW-<br>ID:P54876<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE II (EC<br>6.3.5.3) (FGAM SYNTHASE II) -<br>MYCOBACTERIUM<br>TUBERCULOSIS, 754 aa.  | 2.80E-72                   |                |
| 867 | cg44027791 | 1261 | GAAGCGCTTCT<br>GACACTGGGCG<br>CAC[T/C]CGAAG<br>CGTTGTCCCTT<br>GTGTGGGT  | T | C | Glu | Gly<br>(1240) | NON-<br>CONSERVATI<br>VE | transcript<br>factor | Human Gene SWISSPROT-<br>ID:Q02086 TRANSCRIPTION<br>FACTOR SP2 (KIAA0048) - HOMO<br>SAPIENS (HUMAN), 606 aa.  | 0.00E+00                   | 17             |

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| 868 | cg43992817 | 578  | GAGGGGCCGCT<br>GGAAGGTGACA<br>CTG[C/T]GTTGG<br>GGCCACGGAG<br>GTGCCGCTG   | C | T | Ala | Thr<br>(1241) | NON-<br>CONSERVATIVE | transcript<br>factor | Human Gene Homologous to<br>SWISSNEW-ID:Q14469<br>TRANSCRIPTION FACTOR HES-1<br>(HAIRY AND ENHANCER OF SPLIT<br>1) (HAIRY- LIKE) (HHL) (HAIRY<br>HOMOLOG) - HOMO SAPIENS<br>(HUMAN), 280 aa.   | 1.50E-144 | 3        |
| 869 | cg43297259 | 816  | TAAGTGCTCTGAT<br>GAGGTGIGACT<br>TC[T/C]GGCTAA<br>AGCCTTGCTCA<br>CACTCCCT | T | C | Gln | Arg<br>(1242) | NON-<br>CONSERVATIVE | transcript<br>factor | Human Gene Similar to SWISSNEW-<br>ID:Q61751 RENAL TRANSCRIPTION<br>FACTOR KID-1 (TRANSCRIPTION<br>FACTOR 17) - MUS MUSCULUS<br>(MOUSE), 572 aa.   pcsl:SWISSPROT-<br>ID:Q61751 RENAL TRANSCRIPTION<br>FACTOR KID-1 (TRANSCRIPTION<br>FACTOR 17) - MUS MUSCULUS<br>(MOUSE), 572 aa.                                      | 7.80E-54  |          |
| 870 | cg42716761 | 1594 | CGAGAAAGACCC<br>TATACCATCACG<br>TG[C/G]ACGGCT<br>GCGACGTGTC<br>CACCTCCG  | C | G | His | Asp<br>(1243) | NON-<br>CONSERVATIVE | transcript<br>factor | Human Gene SWISSNEW-ID:Q61079<br>SINGLE-MINDED HOMOLOG 2 (SIM<br>TRANSCRIPTION FACTOR) (MSIM) -<br>MUS MUSCULUS (MOUSE), 657<br>aa.   pcsl:SWISSPROT-ID:Q61079<br>SINGLE-MINDED HOMOLOG 2 (SIM<br>TRANSCRIPTION FACTOR) (MSIM) -<br>MUS MUSCULUS (MOUSE), 657 aa.  | 5.7e-312  | 21       |
| 871 | cg42166807 | 2828 | AGAGCAATGGC<br>TCTCTTCACTCC<br>GT[G/A]GAAGTT<br>GTCCTCTCAGAA<br>GCTGGGC  | G | A | Trp | End<br>(1244) | NON-<br>CONSERVATIVE | transferase          | Human Gene SWISSPROT-<br>ID:Q09328 ALPHA-1,3(6)-<br>MANNOSYLGLYCOPROTEIN BETA-<br>1,6-N-ACETYL-<br>GLUCOSAMINYLTRANSFERASE V<br>(EC 2.4.1.155) (ALPHA-MANNOSIDE<br>BETA-1,6-N-<br>ACETYLGLUCOSAMINYLTRANSFE<br>RASE) (N-ACETYLGLUCOSAMINYL-<br>TRANSFERASE V) (GNT-V)<br>(GLCNAC-T V) - HOMO SAPIENS<br>(HUMAN), 741 aa. | 0.00E+00  | 2 (2q21) |

|     |            |      |   |   |   |     |               |                          |           |  |           |          |
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| 872 | cg38869466 | 752  | TTCACCTGTATT<br>AACGTCCTGGT<br>CCGTCGGGCTT<br>CATAATGGTGTC<br>AGGATTT   | T | C | Leu | Pro<br>(1245) | NON-<br>CONSERVATI<br>VE | transport | Human Gene SWISSPROT-<br>ID:P30825 HIGH-AFFINITY<br>CATIONIC AMINO ACID<br>TRANSPORTER-1 (CAT-1) (CAT1)<br>(SYSTEM Y+ BASIC AMINO ACID<br>TRANSPORTER) (ECOTROPIC<br>RETROVIRAL LEUKEMIA<br>RECEPTOR HOMOLOG) (ERR)<br>(ECOTROPIC RETROVIRUS<br>RECEPTOR HOMOLOG) - HOMO<br>SAPIENS (HUMAN), 629 aa. | 0.00E+00  | 13       |
| 873 | cg42742340 | 3392 | CAGAGAGACGG<br>TGTCATCAGCA<br>TCGTCGGCCT<br>CCCTGCAGCAG<br>ACCCAGGC     | C | T | Arg | Trp<br>(1246) | NON-<br>CONSERVATI<br>VE | transport | Human Gene SWISSPROT-<br>ID:Q04671 P PROTEIN<br>(MELANOCYTE-SPECIFIC<br>TRANSPORTER PROTEIN) - HOMO<br>SAPIENS (HUMAN), 838 aa.  | 0.00E+00  | 15       |
| 874 | cg43976701 | 513  | TGGTATATCTGA<br>ACTGAATCAGC<br>CTGTCCTGAAC<br>TTTTACCTCAGT<br>TTTCTAG   | G | C | Ala | Pro<br>(1247) | NON-<br>CONSERVATI<br>VE | transport | Human Gene SWISSPROT-<br>ID:Q15436 PROTEIN TRANSPORT<br>PROTEIN SEC23 HOMOLOG<br>ISOFORM A - HOMO SAPIENS<br>(HUMAN), 765 aa.  | 0.00E+00  |          |
| 875 | cg43920728 | 2024 | GTAAGTCTCATT<br>GTAAATTTGTTG<br>C[A/G]TGAGCAG<br>TGCTGGGGAGT<br>TGACAGC | A | G | Cys | Arg<br>(1248) | NON-<br>CONSERVATI<br>VE | transport | Human Gene SWISSPROT-<br>ID:P22732 GLUCOSE<br>TRANSPORTER TYPE 5, SMALL<br>INTESTINE (FRUCTOSE<br>TRANSPORTER) - HOMO SAPIENS<br>(HUMAN), 501 aa.  | 2.90E-237 | 1 (1p31) |
| 876 | cg43920728 | 2185 | TGCTTGCTCTG<br>GAAGGGCAGAG<br>TGCTCTGCTCA<br>CCTCCTTTTAGC<br>CAAAGTAA   | C | T | Arg | Gln<br>(1249) | NON-<br>CONSERVATI<br>VE | transport | Human Gene SWISSPROT-<br>ID:P22732 GLUCOSE<br>TRANSPORTER TYPE 5, SMALL<br>INTESTINE (FRUCTOSE<br>TRANSPORTER) - HOMO SAPIENS<br>(HUMAN), 501 aa.  | 2.90E-237 | 1 (1p31) |

|     |            |      |   |   |   |     |               |                          |                  |  |          |                      |
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| 877 | cg42339179 | 450  | TCCTCCACCAG<br>GGTCATTTGCG<br>GT[G/A]TTTAAAA<br>GTTCCAGTGATC<br>TCAATG    | G | A | His | Tyr<br>(1250) | NON-<br>CONSERVATI<br>VE | transport        | Human Gene Homologous to<br>SWISSNEW-ID:Q60714 LONG-<br>CHAIN FATTY ACID TRANSPORT<br>PROTEIN (FATP) - MUS MUSCULUS<br>(MOUSE), 646 aa.   pcis:SWISSPROT-<br>ID:Q60714 LONG-CHAIN FATTY<br>ACID TRANSPORT PROTEIN<br>(FATP) - MUS MUSCULUS<br>(MOUSE), 646 aa. | 1.90E+05 | 15                   |
| 878 | cg17663981 | 383  | TGCACCTGCGA<br>CCAAAACCCCT<br>GCA[G/A]CTGCC<br>CCAAAGGGGAT<br>GTCAACTAC   | G | A | Ser | Asn<br>(1251) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:Q05329 GLUTAMATE<br>DECARBOXYLASE, 65 KD<br>ISOFORM (EC 4.1.1.15) (GAD-65)<br>(65 KD GLUTAMIC ACID<br>DECARBOXYLASE) - Homo sapiens<br>(Human), 585 aa.   | 0.00E+00 | 10<br>(10p11.2<br>3) |
| 879 | cg43918356 | 1806 | GCTCCCTGTGCA<br>CGGGGCTGTAG<br>CGC[C/T]CAGGA<br>CTGCCACAGGCC<br>TGGCTTTGC | C | T | Gly | Glu<br>(1252) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75176 KIAA0692 PROTEIN -<br>HOMO SAPIENS (HUMAN), 783 aa<br>(fragment).   | 0.00E+00 | 12                   |
| 880 | cg43924089 | 1080 | ACCTCCTGGAG<br>CAGTCCTGGTG<br>TTA[C/T]ATTCCC<br>TGCCCTGGAG<br>TTCCCACT    | C | T | His | Tyr<br>(1253) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA31589 KIAA0614 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1630 aa<br>(fragment).   | 0.00E+00 | 12                   |
| 881 | cg43930961 | 2459 | TTCTCCGTAGT<br>CACAGACGTTA<br>GG[C/T]TACTGC<br>TTTCGGCTTCAA<br>TGGAAAC    | C | T | Ser | Asn<br>(1254) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA20772 KIAA0313 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1499 aa.   | 0.00E+00 | 4                    |
| 882 | cg43966528 | 680  | AACAACACATTC<br>AGTACAGTGCA<br>GC[A/G]TATCAG<br>CAGGCCAAGTT<br>AACCAATC   | A | G | Met | Thr<br>(1255) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O00237 HKF-1 - HOMO<br>SAPIENS (HUMAN), 685 aa.  | 0.00E+00 |                      |





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|-----|------------|------|--|---|---|-----|---------------|--------------------------|------------------|---|-----------|----|
| 890 | cg44002507 | 507  | CGCAGGTCCTG<br>GTGGGCCATGA<br>ACA[C/T]GCGCA<br>CGGGCACCAGG<br>TTGGGCTCG  | C | T | Val | Met<br>(1263) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD21812 G9A - HOMO<br>SAPIENS (HUMAN), 1001 aa.   | 8.10E-298 |    |
| 891 | cg44128920 | 1086 | GAGCAGCAGCG<br>AAAACGGCTTCA<br>AC[A/C]GCAGTT<br>GGAAGAACGCA<br>GTCGTGAA  | A | C | Gln | Pro<br>(1264) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O15184 CDC42-INTERACTING<br>PROTEIN 4 - HOMO SAPIENS<br>(HUMAN), 545 aa.  | 1.00E-290 | 19 |
| 892 | cg43968641 | 3315 | TCATTCATCTCA<br>GGGAACATATC<br>AG[C/T]CAGAGA<br>AATATACAAGAA<br>CATTCTCT | C | T | Ala | Thr<br>(1265) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q15043 MRNA (KIAA0062) FOR<br>ORF (NOVEL PROTEIN), PARTIAL<br>CDS - HOMO SAPIENS (HUMAN),<br>531 aa (fragment). | 2.00E-285 | 8  |
| 893 | cg43934178 | 2180 | ACAAAGTAGTG<br>GAACTTCCCTTT<br>GA[A/G]CACGTC<br>CAGGGTGTGGC<br>CCAGGACC  | A | G | Phe | Leu<br>(1266) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD29670 DNA<br>TOPOISOMERASE III BETA - HOMO<br>SAPIENS (HUMAN), 862 aa.                                      | 1.80E-274 |    |
| 894 | cg43934178 | 2596 | CCAGGGCATGA<br>CCTCCGTGAAG<br>CCT[G/A]GTGAG<br>AGGACGGTCTT<br>CCCGGAGCA  | G | A | Pro | Leu<br>(1267) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD29670 DNA<br>TOPOISOMERASE III BETA - HOMO<br>SAPIENS (HUMAN), 862 aa.                                      | 1.80E-274 |    |
| 895 | cg43949042 | 378  | GGACGTACATG<br>AGGACGGCTAT<br>TGG[C/A]GTCC<br>GATGATGAGCG<br>ACAGCCACA   | C | A | Gln | His<br>(1268) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75907 ACAT RELATED GENE<br>PRODUCT 1 - HOMO SAPIENS<br>(HUMAN), 488 aa.  | 6.10E-268 |    |
| 896 | cg43916582 | 2097 | CCTTCATCTTTA<br>TTCTGCTGCTCA<br>GT[G/T]TCCATTT<br>GTTCTCTTTGAT<br>TGGCT  | T | G | Thr | Pro<br>(1269) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75475 LENS EPITHELIUM-<br>DERIVED GROWTH FACTOR -<br>HOMO SAPIENS (HUMAN), 530 aa.                             | 2.30E-259 |    |

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| 897 | cg43258841 | 485  | AACTCCATCCAC<br>AAGTCCCTTGCTG<br>A[A/G]TAATCAAT<br>CGCTGAGCCTC<br>ATCTCT | A | G | Ile<br>(1270) | Thr<br>(1270) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q14449 GROWTH FACTOR<br>RECEPTOR-BOUND PROTEIN 14<br>(GRB14 ADAPTER PROTEIN) -<br>Homo sapiens (Human), 540 aa.<br>Human Gene SPTREMBL-<br>ACC:Q13977 MAJOR YO<br>PARANEOPLASTIC ANTIGEN -<br>HOMO SAPIENS (HUMAN), 509 aa<br>(fragment). | 2.70E-258 |                 |
| 898 | cg43979679 | 619  | GAGAAAGGAGCC<br>CGGAAAGTGT<br>GAC[C/T]AGGAG<br>AAACCGGCACC<br>CAGCTTTGC  | C | T | Gln<br>(1271) | End<br>(1271) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q13977 MAJOR YO<br>PARANEOPLASTIC ANTIGEN -<br>HOMO SAPIENS (HUMAN), 509 aa<br>(fragment).  | 5.60E-258 | 16<br>(16p13.1) |
| 899 | cg42202923 | 887  | TACCCCAATGGT<br>CTTCAGCCTCTG<br>C[A/G]GCAGCTC<br>CGATGAGGTCA<br>GCTGCCG  | A | G | Leu<br>(1272) | Pro<br>(1272) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75926 PROTEIN INHIBITOR<br>OF ACTIVATED STAT PROTEIN<br>PIASY - HOMO SAPIENS (HUMAN),<br>510 aa.   | 2.40E-256 |                 |
| 900 | cg43320405 | 994  | CCAGGCCCTCGA<br>ATGGACAGCAC<br>CTT[C/A]ATGATG<br>GGTCTGTGGTG<br>GCTCAGGC | C | A | Met<br>(1273) | Ile<br>(1273) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:CAB46424 DKFZP434G153<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 466 aa.  | 8.20E-245 |                 |
| 901 | cg43917689 | 3689 | TGACAACGCAG<br>GCTCCAGGGGT<br>TGT[G/A]GCTGA<br>TCTTCTCAGAAC<br>TCAAGCCA  | G | A | His<br>(1274) | Tyr<br>(1274) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q92551 MYELOBLAST<br>KIAA0263 - HOMO SAPIENS<br>(HUMAN), 441 aa.  | 3.50E-240 | 3               |
| 902 | cg43922856 | 1546 | GAGAATTCAGT<br>GATTGGCAGAA<br>TAG[G/A]AGATG<br>CATGCTTGAAT<br>TTCCAGTC   | G | A | Pro<br>(1275) | Ser<br>(1275) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P42167 THYMOPOIETINS<br>BETA AND GAMMA (TP BETA AND<br>TP GAMMA) - Homo sapiens<br>(Human), 453 aa.  | 2.00E-237 | 12<br>(12q22)   |
| 903 | cg43922856 | 1608 | AACTAAGGATTCA<br>GTTGCTTGAAG<br>CC[A/T]TTATAGT<br>TTCAGCTATGG<br>GAGTACT | A | T | Met<br>(1276) | Lys<br>(1276) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P42167 THYMOPOIETINS<br>BETA AND GAMMA (TP BETA AND<br>TP GAMMA) - Homo sapiens<br>(Human), 453 aa.  | 2.00E-237 | 12<br>(12q22)   |



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| 911 | cg43996402 | 684  | CTTCTCCGGCT<br>CCTTTCCTCCCT<br>GC[C/A]GTGGCT<br>TCTGCTGCTCC<br>CCTCCCTT  | C | A | Gly | Cys<br>(1284) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q12804 RECEPTIN - HOMO<br>SAPIENS (HUMAN), 451 aa.  | 2.60E-189 | 2  |
| 912 | cg43984909 | 1268 | CGAATATCAGCT<br>GCATCCAGTGT<br>CC[C/T]CAGACG<br>AGAATACAAGC<br>CAAGGCCT  | C | T | Pro | Leu<br>(1285) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q99963 PROTEIN<br>CONTAINING SH3 DOMAIN,<br>SH3GL3 - HOMO SAPIENS<br>(HUMAN), 347 aa.   | 1.70E-187 | 15 |
| 913 | cg42910688 | 778  | GACAGAGGACA<br>TTCCCATAAATT<br>TG[G/T]TTGGCA<br>ACAAAAGTGACT<br>TAGTGCG  | G | T | Val | Phe<br>(1286) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P55040 GTP-BINDING<br>PROTEIN GEM (GTP-BINDING<br>MITOGEN-INDUCED T-CELL<br>PROTEIN) (RAS-LIKE PROTEIN KIR)<br>- Homo sapiens (Human), 296 aa. | 7.70E-158 | 8  |
| 914 | cg43950590 | 1351 | AAGAACTCCTCC<br>GACGGCTTCGT<br>TAC[C/T]ATCCTG<br>TCTGAAGCGGA<br>TTGCACGA | C | T | Gly | Ser<br>(1287) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75323 GBAS - HOMO<br>SAPIENS (HUMAN), 286 aa.  | 1.90E-154 | 7  |
| 915 | cg44931503 | 945  | TTTTAAAGAGTT<br>CATATAATCATA<br>G[A/G]GGTCTTC<br>AAATACCGTTGT<br>TCCTTC  | A | G | Leu | Pro<br>(1288) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD34078 CGI-83 PROTEIN -<br>HOMO SAPIENS (HUMAN), 288 aa.   | 5.00E-154 |    |
| 916 | cg43303845 | 774  | ACATTGCCTAGA<br>CAAAACTCACAA<br>C[T/C]ACCTGCT<br>CAAGTTCAAAAT<br>GGCCCA  | T | C | Leu | Pro<br>(1289) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O93263 AVENA -<br>GALLUS GALLUS (CHICKEN), 550<br>aa.  | 1.90E-138 |    |
| 917 | cg43973762 | 117  | AGCTGAACAAC<br>AGAAATTGTGG<br>AAT[G/T]AGGAG<br>TTAAAATATGCC<br>AGAGGCCAA | G | T | Glu | End<br>(1290) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O14777<br>RETINOBLASTOMA-ASSOCIATED<br>PROTEIN HEC - HOMO SAPIENS<br>(HUMAN), 642 aa.  | 2.20E-137 |    |

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| 918 | cg43973762 | 165 | CAAGAAGCGA<br>TTGAACACAAAT<br>TA[G/C]CAGAGT<br>ATCACAAATTGG<br>CTAGAAA   | G | C | Ala | Pro<br>(1291) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O14777<br>RETINOBLASTOMA-ASSOCIATED<br>PROTEIN HEC - HOMO SAPIENS<br>(HUMAN), 642 aa.  | 2.20E-137 |  |
| 919 | cg43973762 | 376 | GCCCTAAATAAA<br>AAATGGGTTTG<br>G[A/G]GGATACT<br>TTAGAACAAATTG<br>AATGCA  | A | G | Glu | Gly<br>(1292) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O14777<br>RETINOBLASTOMA-ASSOCIATED<br>PROTEIN HEC - HOMO SAPIENS<br>(HUMAN), 642 aa.  | 2.20E-137 |  |
| 920 | cg42910848 | 443 | CCATGGTGCCA<br>GGCCGTGCTCC<br>CCA[G/C]GTGCC<br>TCCGGGGTGCT<br>GAAGATCTT  | G | C | Pro | Arg<br>(1293) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O14988 GTPASE-<br>ACTIVATING PROTEIN - HOMO<br>SAPIENS (HUMAN), 308 aa<br>(fragment).  | 3.10E-132 |  |
| 921 | cg29351416 | 537 | TTTCCCAAAAGT<br>TCCAAAGTAGACA<br>A[C/G]AGTAATC<br>GCCTGTTACTG<br>CAGCAGG | C | G | Asn | Lys<br>(1294) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q03626 ALPHA-1-<br>INHIBITOR III PRECURSOR,<br>ISOFORM 2 (RAT PLASMA<br>PROTEINASE INHIBITOR ALPHA-1-<br>INHIBITOR III GROUP 3 VARIANT<br>36A) (ALPHA-1 PROTEINASE<br>INHIBITOR 3, EXONS 1-4) - RATTUS<br>NORVEGICUS (RAT), 1487 aa. | 3.20E-127 |  |
| 922 | cg29351416 | 574 | GTTACTGCAGC<br>AGGTCTCATTAC<br>CA[G/T]JACATTC<br>CTGGGAACTATA<br>CCGTCAG | G | T | Asp | Tyr<br>(1295) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q03626 ALPHA-1-<br>INHIBITOR III PRECURSOR,<br>ISOFORM 2 (RAT PLASMA<br>PROTEINASE INHIBITOR ALPHA-1-<br>INHIBITOR III GROUP 3 VARIANT<br>36A) (ALPHA-1 PROTEINASE<br>INHIBITOR 3, EXONS 1-4) - RATTUS<br>NORVEGICUS (RAT), 1487 aa. | 3.20E-127 |  |
| 923 | cg43938372 | 481 | TGTTTCCCACT<br>TAATTTATTTTT<br>[C/T]CTGCTTGT<br>CTTCTGTTTCA<br>TCCT      | C | T | Gly | Glu<br>(1296) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAD40376<br>PTD013 - HOMO SAPIENS<br>(HUMAN), 243 aa.   | 1.50E-123 |  |

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| 924 | cg44930828 | 658 | CCTCAAGGTTTC<br>GCTGCCGAAGC<br>TT[G/A]CCAACG<br>TGCAGCTCCTG<br>GATACCGA  | G | A | Ala | Thr<br>(1297) | NON-<br>CONSERVATIVE | UNCLASSIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:Q29459<br>PLATELET-ACTIVATING FACTOR<br>ACETYLHYDROLASE IB BETA<br>SUBUNIT (EC 3.1.1.47) (PAF<br>ACETYLHYDROLASE 30 KD<br>SUBUNIT) (PAF-AH 30 KD<br>SUBUNIT) (PAF-AH BETA SUBUNIT)<br>- Homo sapiens (Human), and Bos<br>taurus (Bovine), 229 aa. | 3.10E-122 |   |
| 925 | cg44930828 | 680 | CTTGCCAAACGT<br>GCAGCTCCTGG<br>ATA[C/T]CGACG<br>GGGGTTTTGTG<br>CACTCGGAC | C | T | Thr | Ile<br>(1298) | NON-<br>CONSERVATIVE | UNCLASSIFIED | Human Gene Homologous to<br>SWISSNEW-ACC:Q29459<br>PLATELET-ACTIVATING FACTOR<br>ACETYLHYDROLASE IB BETA<br>SUBUNIT (EC 3.1.1.47) (PAF<br>ACETYLHYDROLASE 30 KD<br>SUBUNIT) (PAF-AH 30 KD<br>SUBUNIT) (PAF-AH BETA SUBUNIT)<br>- Homo sapiens (Human), and Bos<br>taurus (Bovine), 229 aa. | 3.10E-122 |   |
| 926 | cg44035718 | 919 | CTGGAGTACCA<br>GGAAGAACTGA<br>GGT[C/T]CCACT<br>ACAAGGACATG<br>CTCAGCGAA  | C | T | Ser | Phe<br>(1299) | NON-<br>CONSERVATIVE | UNCLASSIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:BAA83010<br>KIAA1058 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1534 aa<br>(fragment).   | 2.20E-121 | 2 |
| 927 | cg44921277 | 571 | TTGGCGCAACTT<br>CCCCATCACCTT<br>C[G/A]CCTGCTA<br>TGCGGCCCTCT<br>TCTGCCT  | G | A | Ala | Thr<br>(1300) | NON-<br>CONSERVATIVE | UNCLASSIFIED | Human Gene Homologous to<br>SWISSPROT-ACC:Q35682<br>MYELOID UPREGULATED PROTEIN<br>- Mus musculus (Mouse), 296 aa.   | 1.70E-120 |   |
| 928 | cg43250166 | 461 | GCCGTGATTG<br>CTCCAGTGCCA<br>TCT[C/T]GTGCA<br>GATGCTCATCTC<br>GGCTCTCG   | C | T | Glu | Lys<br>(1301) | NON-<br>CONSERVATIVE | UNCLASSIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:CAB43382<br>HYPOTHETICAL 146.2 KD PROTEIN<br>- HOMO SAPIENS (HUMAN), 1296<br>aa.   | 3.30E-102 | 2 |

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| 929 | cg39512856 | 344 | CTTTTCCAGGC<br>TTCAGCAACG<br>AG[G/A]TTCTTC<br>CTTCGTTGCAAT<br>TTCCAG     | G | A | Thr | Ile<br>(1302) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.                 | 1.20E-98 |                |
| 930 | cg39512856 | 517 | GCCGTTCCACCT<br>CTGATATCCCC<br>TTC/TCCGGCGA<br>TAACCAGGTAA<br>ATTTTC     | C | T | Gly | Glu<br>(1303) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.                 | 1.20E-98 |                |
| 931 | cg39512856 | 536 | TCCCTCCCCG<br>CGATAACCCAG<br>TAA[A/C]ATTTTC<br>CGGTAACGGAC<br>CGAGTTCA   | A | C | Phe | Val<br>(1304) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.                 | 1.20E-98 |                |
| 932 | cg39512856 | 638 | TGGTCTTCAACG<br>AGATGCCACGA<br>TG[C/A]CTCATC<br>ACTGTTGAAAC<br>AGCCACA   | C | A | Ala | Ser<br>(1305) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P03740 HYPOTHETICAL<br>PROTEIN ORF194 - Bacteriophage<br>lambda, 194 aa.                 | 1.20E-98 |                |
| 933 | cg39570960 | 851 | GCCTCCAGGAA<br>GTCGTTTGTGTT<br>TG[A/G]GCTGAA<br>CGAATGTGCGT<br>CCAGCCGC  | A | G | Glu | Gly<br>(1306) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O14997 3-7 GENE PRODUCT -<br>HOMO SAPIENS (HUMAN), 709 aa<br>(fragment).                  | 2.60E-93 |                |
| 934 | cg43980391 | 510 | AGTAAATGGACA<br>AGAATATCATCT<br>T[C/T]AACTTGTA<br>GACACAGCCGG<br>GCAAGA  | C | T | Gln | End<br>(1307) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q15382 RAS-RELATED GTP-<br>BINDING PROTEIN - HOMO<br>SAPIENS (HUMAN), 184 aa.             | 2.10E-90 | 1              |
| 935 | cg43983527 | 991 | TTCTGGAAGGAT<br>GGTGCACCCCTG<br>GT[G/T]CGGCCG<br>CCATTACTGCCA<br>GAGTCTG | G | T | Cys | Phe<br>(1308) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P47226 TESTIN 2 (TES2)<br>[CONTAINS: TESTIN 1 (TES1)] - Mus<br>musculus (Mouse), 423 aa. | 6.50E-90 | 3<br>(11q23.3) |





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| 943 | cg43918287 | 676  | TAAACAGCCC<br>AGCCGCCAAC<br>CCC[A/G]AAAGT<br>TGGCTGCAGTT<br>ATATTAAT     | A | G | Leu | Ser<br>(1316) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P87891 GAG PROTEIN -<br>HUMAN ENDOGENOUS<br>RETROVIRUS K, 426 aa (fragment).  | 7.30E-84 |    |
| 944 | cg43918287 | 693  | CAACCCCAAA<br>AGTTGGTCTGC<br>AGTT[C]ATATTA<br>ATTGAGGTTGG<br>ACCTGGG     | T | C | Ile | Met<br>(1317) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:P87891 GAG PROTEIN -<br>HUMAN ENDOGENOUS<br>RETROVIRUS K, 426 aa (fragment).  | 7.30E-84 |    |
| 945 | cg37027086 | 217  | GAATCAGAACTA<br>CAAGGATCAATT<br>A[T/C]CCCAGCT<br>CAATGTCAGGG<br>TTCTTCA  | T | C | Ser | Pro<br>(1318) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA76824<br>KIAA0980 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1406 aa<br>(fragment).  | 1.20E-83 |    |
| 946 | cg42688841 | 430  | ATTATAACTGGG<br>ATCCCAAGTCAAC<br>A[T/A]AAGGTAG<br>AATTCATTAAAC<br>CTCAAG | T | A | Met | Leu<br>(1319) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:Q02380 NADH-UBIQUINONE<br>OXIDOREDUCTASE SGD<br>SUBUNIT PRECURSOR (EC 1.6.5.3)<br>(EC 1.6.99.3) (COMPLEX I-SGDH)<br>(CI-SGDH) - Bos taurus (Bovine), 189<br>aa. | 1.90E-83 |    |
| 947 | cg42688841 | 598  | CCGAGCCTAGT<br>GCCAGCGCGGC<br>GGC[A/C]AGACA<br>GAGCTGTCAGA<br>GCGGCGACC  | A | C | Cys | Gly<br>(1320) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:Q02380 NADH-UBIQUINONE<br>OXIDOREDUCTASE SGD<br>SUBUNIT PRECURSOR (EC 1.6.5.3)<br>(EC 1.6.99.3) (COMPLEX I-SGDH)<br>(CI-SGDH) - Bos taurus (Bovine), 189<br>aa. | 1.90E-83 |    |
| 948 | cg40332814 | 339  | ACTGCACAGGG<br>ACCGAATCTCTG<br>CC[T/C]CCCCGCT<br>CTGCAGCCAGG<br>TGCTCCAA | T | C | Glu | Gly<br>(1321) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA74864<br>KIAA0841 PROTEIN - HOMO<br>SAPIENS (HUMAN), 641 aa<br>(fragment).   | 3.10E-83 | 19 |
| 949 | cg43920571 | 2059 | GCGTTTTTCTCT<br>CACGTCCTGCT<br>GA[G/A]ATTACT<br>GAGGAATATTGT<br>GCTGGC   | G | A | Ser | Phe<br>(1322) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P34624 HYPOTHETICAL 63.5<br>KD PROTEIN ZK353.1 IN<br>CHROMOSOME III - Caenorhabditis<br>elegans, 548 aa.   | 3.50E-82 | 10 |

|     |            |     |  |   |   |     |               |                          |                  |  |          |          |
|-----|------------|-----|--|---|---|-----|---------------|--------------------------|------------------|--|----------|----------|
| 950 | cg44024149 | 451 | GGAAGCCGCAC<br>TCAGTTATGGCT<br>TC[T/C]ACGGCT<br>GCCACTGTGGC<br>GTGGGTGG  | T | C | Tyr | His<br>(1323) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P14555 PHOSPHOLIPASE A2,<br>MEMBRANE ASSOCIATED<br>PRECURSOR (EC 3.1.1.4)<br>(PHOSPHATIDYLCHOLINE 2-<br>ACYLHYDROLASE) (GROUP II<br>PHOSPHOLIPASE A2) - Homo<br>sapiens (Human), 144 aa. | 5.30E-79 | 1 (1p35) |
| 951 | cg43307245 | 156 | GATATGATAGCT<br>TGTCCTGAAACT<br>G[A/G]GACTCCT<br>GCCGTGATAAC<br>GTGTGAC  | A | G | Glu | Gly<br>(1324) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O15488 GLYCOGENIN-2<br>ALPHA - HOMO SAPIENS (HUMAN),<br>501 aa.   | 1.00E-75 | X        |
| 952 | cg39523553 | 698 | GTGTGAGGTCT<br>GCCCGATCCGG<br>GAT[G/A]GCTGC<br>CGGTGGGTGAT<br>CGACGGTAG  | G | A | Gly | Ser<br>(1325) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa.   | 7.20E-75 |          |
| 953 | cg39523553 | 861 | ATGGCTCTTTCC<br>GCCTGGCCCCGA<br>GC[T/C]CGATCA<br>GGCATCAAGGT<br>GCCTGGAA | T | C | Leu | Pro<br>(1326) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa.   | 7.20E-75 |          |
| 954 | cg35933325 | 312 | ACCAAATGCCA<br>CTATTTTTCTC<br>CC[A/C]TTGCCA<br>AAAATGAAGGAA<br>ATCACGT   | A | C | Asn | Lys<br>(1327) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA74845<br>KIAA0822 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1581 aa.  | 2.40E-74 |          |
| 955 | cg41677120 | 325 | CACGACCCACG<br>AGATCATGGGG<br>CCC[A/G]AGAAA<br>AAGCACCTGGA<br>CTACTTAAT  | A | G | Lys | Glu<br>(1328) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q13492 CALM (TYPE I CALM<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 652 aa.   | 1.10E-71 | 11       |

|     |            |     |  |   |   |     |               |                          |                  |   |          |    |
|-----|------------|-----|--|---|---|-----|---------------|--------------------------|------------------|---|----------|----|
| 956 | cg41677120 | 330 | CCCACGAGATC<br>ATGGGGCCCAA<br>GAA/CJAAGCA<br>CCTGGACTACTT<br>AATTCAGT    | A | C | Lys | Asn<br>(1329) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q13492 CALM (TYPE I CALM<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 652 aa.                          | 1.10E-71 | 11 |
| 957 | cg41677120 | 382 | CACAAATGAGAT<br>GAATGTGAACAT<br>C[C/T]CACAGTT<br>GGCAGACAGTT<br>TAATTTGA | C | T | Pro | Ser<br>(1330) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q13492 CALM (TYPE I CALM<br>PROTEIN) - HOMO SAPIENS<br>(HUMAN), 652 aa.                          | 1.10E-71 | 11 |
| 958 | cg39648832 | 208 | TGCAGCCTCGT<br>CCTCCTCCTCTG<br>GC[A/T]GGCTCT<br>GCACACTCTGC<br>TCCTGGTA  | A | T | Leu | Gln<br>(1331) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA76807<br>KIAA0963 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1366 aa.                                 | 3.20E-70 |    |
| 959 | cg42696021 | 412 | GACACCCGCAC<br>CCGGGCATGCT<br>TCA[C/G]ACAGT<br>GGCTGTGCCGC<br>CTTCACAAT  | C | G | Thr | Arg<br>(1332) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P55789 AUGMENTER OF<br>LIVER REGENERATION (HERV1<br>PROTEIN) - Homo sapiens (Human),<br>125 aa. | 1.40E-69 |    |
| 960 | cg42696021 | 421 | ACCCGGGCATG<br>CTTCACACAGTG<br>GC[T/C]GTGCCG<br>CCTTCACAATGA<br>AGTGAAC  | T | C | Leu | Pro<br>(1333) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P55789 AUGMENTER OF<br>LIVER REGENERATION (HERV1<br>PROTEIN) - Homo sapiens (Human),<br>125 aa. | 1.40E-69 |    |
| 961 | cg34243633 | 269 | CAGAGATAATG<br>CAGGCCAGGGA<br>GGA[G/C]ATTGC<br>ACTGGATGTCA<br>CCATCATGG  | G | C | Ile | Met<br>(1334) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O88552 CLAUDIN-2 - MUS<br>MUSCULUS (MOUSE), 230 aa.  | 1.30E-68 |    |



|     |            |      |  |   |   |     |               |                          |                  |  |          |   |
|-----|------------|------|--|---|---|-----|---------------|--------------------------|------------------|--|----------|---|
| 968 | cg44938009 | 1289 | GAGTGCACGCA<br>TAAAGATGGAA<br>GAG[G/T]ATGCA<br>CTACTTTCTGAT<br>CCAGTGGA  | G | T | Asp | Tyr<br>(1341) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:Q43182 RHO-GTPASE-<br>ACTIVATING PROTEIN 6 (RHO-<br>TYPE GTPASE-ACTIVATING<br>PROTEIN RHOGAPX-1) - Homo<br>sapiens (Human), 587 aa. | 5.80E-66 | X |
| 969 | cg43949821 | 287  | ATTTTAATTCCT<br>TCCTGTCTACG<br>GC[G/A]GTTGGA<br>CCTCCTGGCTC<br>TCTGCTGT  | G | A | Arg | Cys<br>(1342) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD34394<br>NUCLEAR PORE COMPLEX<br>INTERACTING PROTEIN NPIP -<br>HOMO SAPIENS (HUMAN), 350 aa.                                     | 3.80E-62 |   |
| 970 | cg39516123 | 681  | TGGCTTCGGCT<br>GGCGGGCCATC<br>AAT[C/T]CCAGC<br>ATGGCTGCCCC<br>CAGCAGTCC  | C | T | Pro | Ser<br>(1343) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q04205 TENSIN - Gallus gallus<br>(Chicken), 1744 aa.   | 5.10E-62 |   |
| 971 | cg42731307 | 347  | CGAAAAGCAAA<br>GTGCAGTTTGT<br>GC[T/C]TCGGCT<br>GTTGAGTGGTT<br>CGGGTCCA   | T | C | Ser | Gly<br>(1344) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q99653 CALCIUM-BINDING<br>PROTEIN P22 (CALCIUM-BINDING<br>PROTEIN CHP) - Homo sapiens<br>(Human), 194 aa.                          | 2.60E-61 |   |
| 972 | cg42731307 | 488  | TCTGGAAGAA<br>GGCATTGATGAT<br>CC[G/A]GTCCCC<br>CAGTGGGTTGA<br>TGGCAAGT   | G | A | Arg | Trp<br>(1345) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q99653 CALCIUM-BINDING<br>PROTEIN P22 (CALCIUM-BINDING<br>PROTEIN CHP) - Homo sapiens<br>(Human), 194 aa.                          | 2.60E-61 |   |
| 973 | cg42731307 | 524  | GGTTGATGGC<br>AAGTTCTGGAAT<br>CC[T/C]CTGGAA<br>ATCTCCCGGCT<br>GAGAGTC    | T | C | Arg | Gly<br>(1346) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q99653 CALCIUM-BINDING<br>PROTEIN P22 (CALCIUM-BINDING<br>PROTEIN CHP) - Homo sapiens<br>(Human), 194 aa.                          | 2.60E-61 |   |
| 974 | cg44910937 | 648  | TGCCCTTTGGAAC<br>AGGAATATGAAA<br>A[G/T]AAACTCA<br>GAGCCGAGTTA<br>GTGGAAA | G | T | Lys | Asn<br>(1347) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q20716 F53B7.3 -<br>CAENORHABDITIS ELEGANS, 267<br>aa.  | 2.60E-61 | 3 |

|     |            |      |   |   |   |     |               |                          |                  |   |          |   |
|-----|------------|------|---|---|---|-----|---------------|--------------------------|------------------|---|----------|---|
| 975 | cg43335624 | 149  | TCGAAAGGAAG<br>TGAGTGCAGAT<br>GGG[A/G]AGACC<br>ATCACTGTCACT<br>TTCCTTAA | A | G | Lys | Glu<br>(1348) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q62184 T-COMPLEX PROTEIN<br>10C (TCP-10) - MUS MUSCULUS<br>(MOUSE), 438 aa.            | 7.00E-61 |   |
| 976 | cg43277268 | 448  | CGCTAATGCCA<br>AGAAGGAGATG<br>GTG[C/A]GCTCC<br>AAGCTGCCCAA<br>CAGTGTGCT | C | A | Arg | Ser<br>(1349) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD45423 EH<br>DOMAIN-CONTAINING PROTEIN<br>EHD1 - MUS MUSCULUS (MOUSE),<br>534 aa.    | 3.90E-60 |   |
| 977 | cg44128084 | 724  | CTTGACATCCAG<br>CCAGACGGTTC<br>AG[A/G]ATCAGC<br>GGTCTGTGGT              | A | G | Glu | Gly<br>(1350) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O33196 HYPOTHETICAL 32.9<br>KD PROTEIN - MYCOBACTERIUM<br>TUBERCULOSIS, 307 aa.        | 1.70E-59 |   |
| 978 | cg30455661 | 322  | TTCTCAAGTGGT<br>TTGAAGTCAAC<br>A[G/T]ATTTCAC<br>AGAAGAAATCA<br>GCCCTC   | G | T | Gln | His<br>(1351) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q14185 DOCK180 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1865 aa.                             | 5.20E-58 |   |
| 979 | cg42747615 | 31   | TGTGATAAAAGT<br>CACTTTCAGGC<br>CA[T/C]TCACAG<br>CGAATCTTCAGA<br>CACTTT  | T | C | Ile | Thr<br>(1352) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q14693 HYPOTHETICAL<br>PROTEIN KIAA0188 - Homo sapiens<br>(Human), 899 aa (fragment). | 1.80E-57 |   |
| 980 | cg43153425 | 276  | ACAAATTACTAT<br>GGGTTCTACTG<br>AA[T/G]CTCGGG<br>TTGACTACATGG<br>GCTCAAG | T | G | Ser | Ala<br>(1353) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA83061<br>KIAA1109 PROTEIN - HOMO<br>SAPIENS (HUMAN), 1957 aa<br>(fragment).         | 2.40E-57 |   |
| 981 | cg43968980 | 1093 | TATTTCTGCTT<br>CTCTAACAGCTG<br>A[C/A]TGTGAATT<br>GCTTCCTTGA<br>CTGAAG   | C | A | Ser | Ile<br>(1354) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O60925 PREFOLDIN SUBUNIT<br>1 - HOMO SAPIENS (HUMAN), 122<br>aa.                       | 2.50E-56 | 5 |

|     |            |     |  |   |   |     |               |                          |                  |   |          |    |
|-----|------------|-----|--|---|---|-----|---------------|--------------------------|------------------|---|----------|----|
| 982 | cg30384142 | 173 | GATAGTGGTGT<br>GTGGTGATGCG<br>AGTATTAACCT<br>GACGAATGGTT<br>AGCTGAAAT    | A | T | Lys | End<br>(1355) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P44788 SUN PROTEIN (FMU<br>PROTEIN) - Haemophilus influenzae,<br>451 aa.  | 5.30E-56 |    |
| 983 | cg43957773 | 445 | GGGCTCACCGT<br>AGAGCAACTGC<br>AATC[A]GCTCT<br>GGGCCTGGGCC<br>TGGACAGGA   | C | A | Asp | Tyr<br>(1356) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O43914 DNAX ACTIVATION<br>PROTEIN 12 - HOMO SAPIENS<br>(HUMAN), 113 aa.  | 3.30E-54 | 19 |
| 984 | cg43931038 | 464 | AGGGCAACTTG<br>TGGGCAACCTG<br>GTC[A/C]AGGAA<br>ACCTTGACTTCT<br>TCAAAATTC | A | C | Leu | Trp<br>(1357) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O46082 EG:63B12.2 PROTEIN -<br>DROSOPHILA MELANOGASTER<br>(FRUIT FLY), 254 aa.   | 6.10E-54 | 11 |
| 985 | cg43931038 | 588 | CCTCCCCCCAT<br>GCGATGCCCAA<br>CAC[T/C]TTTGC<br>GAGTGATGGGC<br>TTGAAAGGG  | T | C | Ser | Gly<br>(1358) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O46082 EG:63B12.2 PROTEIN -<br>DROSOPHILA MELANOGASTER<br>(FRUIT FLY), 254 aa.   | 6.10E-54 | 11 |
| 986 | cg43971060 | 686 | CCCACCTCGTT<br>CGTGCTCCAC<br>CCT[C/T]CCCAG<br>CTCCACCGCCT<br>GGTCTTCAG   | C | T | Pro | Ser<br>(1359) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:P31639 SODIUM/GLUCOSE<br>COTRANSPORTER 2<br>(NA+)/GLUCOSE<br>COTRANSPORTER 2 (LOW<br>AFFINITY SODIUM-GLUCOSE<br>COTRANSPORTER) - Homo sapiens<br>(Human), 672 aa. | 4.20E-53 |    |
| 987 | cg44010070 | 541 | TTCTCTGCCGG<br>CACCTACCCGC<br>GCC[T/G]GGAGG<br>AGTACCGCCGG<br>GGCATCTTA  | T | G | Leu | Arg<br>(1360) | NON-<br>CONSERVATI<br>VE | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:O35775 SYNCOLLIN (SIP9) -<br>Rattus norvegicus (Rat), 145 aa.  | 6.40E-51 |    |



|     |            |     |  |   |     |     |               |                      |                           |   |           |               |
|-----|------------|-----|--|---|-----|-----|---------------|----------------------|---------------------------|---|-----------|---------------|
| 988 | cg43298242 | 145 | TCTGTGGCAG<br>GGCTCACAGAG<br>ACG[G/A]GGGTG<br>AGGGAGAGAT<br>CGTGGGTTT    | G | A   | Pro | Leu<br>(1361) | NON-<br>CONSERVATIVE | water_ch<br>annel         | Human Gene SWISSPROT-<br>ID:O14520 AQUAPORIN-7 LIKE<br>(AQUAPORIN ADIPOSE) (AQPAP) -<br>HOMO SAPIENS (HUMAN), 342 aa.   | 1.30E-163 |               |
| 989 | cg43298242 | 163 | AGAGACGGGG<br>TGAGGGGAGAG<br>ATC[G/A]TGGGT<br>TCATGAGATCCC<br>ATCTTGGG   | G | A   | Thr | Met<br>(1362) | NON-<br>CONSERVATIVE | water_ch<br>annel         | Human Gene SWISSPROT-<br>ID:O14520 AQUAPORIN-7 LIKE<br>(AQUAPORIN ADIPOSE) (AQPAP) -<br>HOMO SAPIENS (HUMAN), 342 aa.   | 1.30E-163 |               |
| 990 | cg43300636 | 440 | CCACAGCCGCC<br>ACGCCACCTC<br>CCG[G/gap]CCC<br>AGGCCAGGCC<br>TATGCGCATCA  | G | gap | Gly | Gly<br>(1363) | FRAMESHIFT           | ATPase_<br>associat<br>ed | Human Gene SPTREMBL-ID:Q29466<br>VACUOLAR H+-ATPASE SUBUNIT<br>(EC 3.6.1.34) (H(+)-TRANSPORTING<br>ATP SYNTHASE) (H(+)-<br>TRANSPORTING ATPASE)<br>(MITOCHONDRIAL ATPASE)<br>(CHLOROPLAST ATPASE)<br>(COUPLING FACTORS (F(O), F(1)<br>AND CF(1))) - BOS TAURUS<br>(BOVINE), 838 aa. | 1.70E-175 |               |
| 991 | cg43300636 | 446 | CCGCCACGCC<br>ACCTCCCGGCC<br>CAG[G/gap]CCCA<br>GGCCTATGCGC<br>ATCACCATGG | G | gap | Gly | Gly<br>(1364) | FRAMESHIFT           | ATPase_<br>associat<br>ed | Human Gene SPTREMBL-ID:Q29466<br>VACUOLAR H+-ATPASE SUBUNIT<br>(EC 3.6.1.34) (H(+)-TRANSPORTING<br>ATP SYNTHASE) (H(+)-<br>TRANSPORTING ATPASE)<br>(MITOCHONDRIAL ATPASE)<br>(CHLOROPLAST ATPASE)<br>(COUPLING FACTORS (F(O), F(1)<br>AND CF(1))) - BOS TAURUS<br>(BOVINE), 838 aa. | 1.70E-175 |               |
| 992 | cg43250373 | 193 | CTGTGGGGTTG<br>ACCCAGAACAA<br>AGC[A/gap]TTGC<br>CAGAAACGTTA<br>AGTATGGGA | A | gap | Leu | Cys<br>(1365) | FRAMESHIFT           | ATPase_<br>associat<br>ed | Human Gene Similar to<br>TREMBLNEW-ID:G2921585 ECTO-<br>ATPASE - MUS MUSCULUS<br>(MOUSE), 495 aa.   | 1.40E-100 | 10<br>(10q24) |

|     |            |      |   |   |     |     |               |            |                   |  |           |                 |
|-----|------------|------|---|---|-----|-----|---------------|------------|-------------------|--|-----------|-----------------|
| 993 | cg43132502 | 360  | GGCCCCAGTGC<br>AGTGGGTGGCA<br>CCG[C/gap]CGA<br>GGCTGCTGTTA<br>CGGCTCATCTT | C | gap | Pro | Arg<br>(1366) | FRAMESHIFT | ATPase associated | Human Gene Similar to SP TREMBL-<br>ID:Q15332 GAMMA SUBUNIT OF<br>SODIUM POTASSIUM ATPASE LIKE<br>- HOMO SAPIENS (HUMAN), 126 aa.  | 9.40E-58  | 11              |
| 994 | cg42528468 | 284  | GCTCCTGCCTG<br>GGAACAACCGG<br>AAG[G/gap]TGTA<br>TGAAGTGAGCA<br>ATGTGCAAGA | G | gap | Val | Cys<br>(1367) | FRAMESHIFT | cadherin          | Human Gene Similar to SWISSPROT-<br>ID:P05362 INTERCELLULAR<br>ADHESION MOLECULE-1<br>PRECURSOR (ICAM-1) (MAJOR<br>GROUP RHINOVIRUS RECEPTOR)<br>(CD54) - HOMO SAPIENS (HUMAN),<br>532 aa. | 8.40E-78  | 19<br>(19p13.3) |
| 995 | cg43264626 | 1150 | TTTGCCAGTTTT<br>CTTCTTGAGTTG<br>G[C/gap]CCTCCA<br>GGCACCCACA<br>GAGCTAAA  | C | gap | Gly | Ala<br>(1368) | FRAMESHIFT | cathepsin         | Human Gene SWISSPROT-<br>ID:P43235 CATHEPSIN K<br>PRECURSOR (EC 3.4.22.38)<br>(CATHEPSIN O) (CATHEPSIN X)<br>(CATHEPSIN O2) - HOMO SAPIENS<br>(HUMAN), 329 aa.                             | 4.10E-183 | 1               |
| 996 | cg43132668 | 1893 | CGATGCGTGCC<br>AGGGTGATTCC<br>GGA[G/gap]GCC<br>CGCTGGTGTGT<br>GAGGACCAAGC | G | gap | Gly | Ala<br>(1369) | FRAMESHIFT | cathepsin         | Human Gene Similar to SWISSPROT-<br>ID:P98119 SALIVARY<br>PLASMINOGEN ACTIVATOR ALPHA<br>1 PRECURSOR (EC 3.4.21.68)<br>(DSPA ALPHA-1) - DESMODUS<br>ROTUNDUS (VAMPIRE BAT), 477<br>aa.     | 3.90E-74  | 5 (5q33)        |
| 997 | cg43132668 | 1894 | GATGCGTGCCA<br>GGGTGATTCCG<br>GAG[G/gap]CCC<br>GCTGGTGTGTG<br>AGGACCAAGCT | G | gap | Gly | Ala<br>(1370) | FRAMESHIFT | cathepsin         | Human Gene Similar to SWISSPROT-<br>ID:P98119 SALIVARY<br>PLASMINOGEN ACTIVATOR ALPHA<br>1 PRECURSOR (EC 3.4.21.68)<br>(DSPA ALPHA-1) - DESMODUS<br>ROTUNDUS (VAMPIRE BAT), 477<br>aa.     | 3.90E-74  | 5 (5q33)        |
| 998 | cg44924334 | 198  | AAAGCTAATTGA<br>GACCTATTTCTC<br>C[A/gap]AAAACT<br>ACCAAGACTATG<br>AGTATCT | A | gap | Lys | Lys<br>(1371) | FRAMESHIFT | glycoprotein      | Human Gene Similar to SWISSPROT-<br>ID:Q13491 NEURONAL MEMBRANE<br>GLYCOPROTEIN M6-B - HOMO<br>SAPIENS (HUMAN), 283 aa<br>(fragment).  | 5.60E-76  |                 |

|      |            |      |  |   |     |     |               |            |                |  |           |    |
|------|------------|------|--|---|-----|-----|---------------|------------|----------------|--|-----------|----|
| 999  | cg43303165 | 2549 | GGCCCCCACTA<br>TCAGGGGCCCT<br>GGC[C/gap]TCAA<br>TCACTGAGACC<br>ATCCAAGTCC  | C | gap | Ser | Gln<br>(1372) | FRAMESHIFT | histone        | Human Gene Similar to SWISSPROT-<br>ID:P53973 HISTONE DEACETYLASE<br>HDA1 - SACCCHAROMYCES<br>CEREVISIAE (BAKER'S YEAST), 706<br>aa.   | 4.10E-70  | X  |
| 1000 | cg42489148 | 881  | TGCGAGTGGAT<br>GCGGAACCGGC<br>GCA[G/gap]CAGT<br>CCCTCGGCAGC<br>CAAGTGAAAA  | G | gap | Ser | Thr<br>(1373) | FRAMESHIFT | homeobox       | Human Gene Homologous to<br>SPTREMBL-ID:O00503 CAUDAL-<br>TYPE HOMEBOX PROTEIN 2 -<br>HOMO SAPIENS (HUMAN), 313 aa.  | 6.00E-118 | 13 |
| 1001 | cg43929210 | 483  | TCTGGCTCAGC<br>ATGATGTTCCCT<br>CT[G/gap]GCCTT<br>CAGCCTGCCAC<br>TAAAGAAATG | G | gap | Ala | Ala<br>(1374) | FRAMESHIFT | hydroxysteroid | Human Gene SWISSPROT-<br>ID:P51659 ESTRADIOL 17 BETA-<br>DEHYDROGENASE 4 (EC 1.1.1.62)<br>(17-BETA-HSD 4) (17-BETA-<br>HYDROXYSTEROID<br>DEHYDROGENASE 4) - HOMO<br>SAPIENS (HUMAN), 736 aa. | 0.00E+00  | 5  |
| 1002 | cg44004587 | 1811 | GCTTATTTTCGG<br>TGTTGAATAAGA<br>A[G/gap]ACACTA<br>AAAGCTCGATG<br>CAATAATC  | G | gap | Val | Val<br>(1375) | FRAMESHIFT | isomerase      | Human Gene Homologous to<br>SPTREMBL-ID:Q13907 HOMOLOG<br>OF YEAST IPP ISOMERASE - HOMO<br>SAPIENS (HUMAN), 228 aa.  | 3.00E-123 |    |
| 1003 | cg41501665 | 156  | CGCTTCTCCAA<br>GGTGCTGGAGG<br>AGG[C/gap]GGC<br>GGCCGCCGAGG<br>AGGGCCTGCC   | C | gap | Ala | Gly<br>(1376) | FRAMESHIFT | kinase         | Human Gene Similar to<br>TREMBLNEW-ID:D1025880 ZIP-<br>KINASE - HOMO SAPIENS<br>(HUMAN), 454 aa.   | 2.70E-76  |    |
| 1004 | cg41501665 | 184  | CGGCCGCCGAG<br>GAGGGCCTGCG<br>CGA[G/gap]CTGC<br>AGCGCAGCCGG<br>CGGCTCTGCC  | G | gap | Leu | Cys<br>(1377) | FRAMESHIFT | kinase         | Human Gene Similar to<br>TREMBLNEW-ID:D1025880 ZIP-<br>KINASE - HOMO SAPIENS<br>(HUMAN), 454 aa.   | 2.70E-76  |    |

|      |            |      |   |   |     |     |               |            |                    |  |           |               |
|------|------------|------|---|---|-----|-----|---------------|------------|--------------------|--|-----------|---------------|
| 1005 | cg41501665 | 202  | TGCGCGAGCTG<br>CAGCGCAGCCG<br>GCG[G/gap]CTCT<br>GCCACGAGGAC<br>GTGGAGGCCG   | G | gap | Leu | Ser<br>(1378) | FRAMESHIFT | kinase             | Human Gene Similar to<br>TREMBLNEW-ID:D1025880 ZIP-<br>KINASE - HOMO SAPIENS<br>(HUMAN), 454 aa.   | 2.70E-76  |               |
| 1006 | cg41501665 | 232  | GCCACGAGGAC<br>GTGGAGGCCGCT<br>GGC[C/gap]GCC<br>ATCTACGAGGA<br>GAAGGAGGCCCT | C | gap | Ala | Pro<br>(1379) | FRAMESHIFT | kinase             | Human Gene Similar to<br>TREMBLNEW-ID:D1025880 ZIP-<br>KINASE - HOMO SAPIENS<br>(HUMAN), 454 aa.   | 2.70E-76  |               |
| 1007 | cg43939695 | 342  | CAAGACTGAGA<br>TCAATTGCCCG<br>CGG[C/gap]CGG<br>ACGATGGGAAC<br>CTCTTCCCCCT   | C | gap | Pro | Arg<br>(1380) | FRAMESHIFT | kinasere<br>ceptor | Human Gene SWISSPROT-<br>ID:Q16288 NT-3 GROWTH FACTOR<br>RECEPTOR PRECURSOR (EC<br>2.7.1.112) (TRKC TYROSINE<br>KINASE) (GP145-TRKC) (TRK-C) -<br>HOMO SAPIENS (HUMAN), 839 aa.  | 0.00E+00  | 15<br>(15q25) |
| 1008 | cg29023997 | 199  | TCTGGATGGGA<br>TGGAGCACCAC<br>GTG[C/gap]GCAC<br>CTGCATCCCCA<br>AAGTGGAGCT   | C | gap | Arg | Ala<br>(1381) | FRAMESHIFT | kinasere<br>ceptor | Human Gene SWISSPROT-<br>ID:P36896 SERINE/THREONINE-<br>PROTEIN KINASE RECEPTOR R2<br>PRECURSOR (EC 2.7.1.37) (SKR2)<br>PRECURSOR (EC 2.7.1.37) (SKR2)<br>(ACTIVIN RECEPTOR-LIKE KINASE<br>4) (ALK-4) (ACTR-IB) - HOMO<br>SAPIENS (HUMAN), 505 aa. | 9.30E-280 | 12            |
| 1009 | cg43983535 | 4377 | CTCCAACACAGCT<br>TCTTCACCTTTT<br>T[C/gap]AGAAGG<br>GCTTCTGCAGC<br>TACCAACT  | C | gap | Leu | Leu<br>(1382) | FRAMESHIFT | laminin            | Human Gene SWISSPROT-<br>ID:P24043 LAMININ ALPHA-2 CHAIN<br>PRECURSOR (LAMININ M CHAIN)<br>(MEROSIN HEAVY CHAIN) - HOMO<br>SAPIENS (HUMAN), 3110 aa.   | 0.00E+00  | 6 (6q22)      |
| 1010 | cg42488873 | 480  | TTCCCCCTTAAAT<br>TGGTCAGCATA<br>GT[G/gap]CCCCA<br>TTTTGGGGCATC<br>CTTCAGCT  | G | gap | His | Thr<br>(1383) | FRAMESHIFT | lipase             | Human Gene SWISSPROT-<br>ID:P54317 PANCREATIC LIPASE<br>RELATED PROTEIN 2 PRECURSOR<br>(EC 3.1.1.3) - HOMO SAPIENS<br>(HUMAN), 469 aa.   | 9.80E-261 |               |

|      |            |      |  |   |     |     |               |            |                |   |           |                 |
|------|------------|------|--|---|-----|-----|---------------|------------|----------------|---|-----------|-----------------|
| 1011 | cg42488873 | 494  | GTCAGCATAGT<br>GCCCCATTTTG<br>GGG[C/gap]ATCC<br>TTCAGCTGGAC<br>AAGGGAACA   | C | gap | Cys | Ser<br>(1384) | FRAMESHIFT | lipase         | Human Gene SWISSPROT-<br>ID:P54317 PANCREATIC LIPASE<br>RELATED PROTEIN 2 PRECURSOR<br>(EC 3.1.1.3) - HOMO SAPIENS<br>(HUMAN), 469 aa.  | 9.80E-261 |                 |
| 1012 | cg42488873 | 923  | CACGCGGCCCC<br>CCAGCCTCCTG<br>CCC[G/gap]CCTC<br>CGCGGCCGTGT<br>GCGCGCCCGAG | G | gap | Ala | Gly<br>(1385) | FRAMESHIFT | lipase         | Human Gene SWISSPROT-<br>ID:P54317 PANCREATIC LIPASE<br>RELATED PROTEIN 2 PRECURSOR<br>(EC 3.1.1.3) - HOMO SAPIENS<br>(HUMAN), 469 aa.  | 9.80E-261 |                 |
| 1013 | cg43249083 | 2329 | GGAGCAGCTCC<br>AGGAGACGCTG<br>CTG[C/gap]GGG<br>CTCTTCGGGCT<br>CTGGTGCTGAA  | C | gap | Arg | Gly<br>(1386) | FRAMESHIFT | nucl_rec<br>pt | Human Gene SWISSPROT-<br>ID:P20393 V-ERBA RELATED<br>PROTEIN EAR-1 - HOMO SAPIENS<br>(HUMAN), 614 aa.   | 0.00E+00  | 17<br>(17q11.2) |
| 1014 | cg43991048 | 6644 | TCTTTCTTTTCTT<br>CTTCTTTTTTTT<br>C/gap]TGTTTTT<br>CTGCTTTATCCT<br>CTTCT    | C | gap | Glu | Lys<br>(1387) | FRAMESHIFT | nucl_rec<br>pt | Human Gene SPTREMBL-ID:Q60974<br>NUCLEAR RECEPTOR CO-<br>REPRESSOR - MUS MUSCULUS<br>(MOUSE), 2453 aa.  | 0.00E+00  | 17              |
| 1015 | cg43919677 | 4055 | GAAGAAAAGAA<br>AGAATGCTACTA<br>TA[A/gap]TCTCA<br>ATGACGCCAGT<br>CTCTGTGAT  | A | gap | Asn | Ile<br>(1388) | FRAMESHIFT | oncogen<br>e   | Human Gene SWISSPROT-<br>ID:Q00918 LATENT<br>TRANSFORMING GROWTH<br>FACTOR BETA BINDING PROTEIN 1<br>PRECURSOR (TRANSFORMING<br>GROWTH FACTOR BETA-1<br>BINDING PROTEIN 1) (TGF-BETA1-<br>BP- 1) (TRANSFORMING GROWTH<br>FACTOR BETA-1 MASKING<br>PROTEIN, LARGE SUBUNIT) -<br>RATTUS NORVEGICUS (RAT), 1712<br>aa. | 0         | 2 (2p12)        |



|      |            |      |   |   |     |     |               |            |                   |  |          |               |
|------|------------|------|---|---|-----|-----|---------------|------------|-------------------|--|----------|---------------|
| 1022 | cg44028327 | 904  | ATGCATACATCG<br>ATATTCAGCTAC<br>G[A/gap]ATTGCT<br>TCCTTCTCACAG<br>AACTGTG | A | gap | Ile | Leu<br>(1395) | FRAMESHIFT | protease<br>nhib  | Human Gene SWISSPROT-<br>ID:P01042 KININOGEN, HMW<br>PRECURSOR (ALPHA-2-THIOL<br>PROTEINASE INHIBITOR)<br>(CONTAINS: BRADYKININ) - HOMO<br>SAPIENS (HUMAN), 644 aa.  | 0        | 3 (3q27)      |
| 1023 | cg43940280 | 720  | CCTCGAAGTCT<br>GCCTGGGCACA<br>CAC[C/gap]ACAT<br>GCAGATTTGGT<br>GCTTTCCCA  | C | gap | Gly | Val<br>(1396) | FRAMESHIFT | ribosoma<br>lprot | Human Gene Similar to SWISSPROT-<br>ID:P49207 60S RIBOSOMAL<br>PROTEIN L34 - HOMO SAPIENS<br>(HUMAN), 116 aa.  | 7.6E-56  |               |
| 1024 | cg43974196 | 5050 | GATTCAGGGCG<br>TGCTCTGGGTG<br>AAG[C/gap]CCAC<br>AGGGTTGAGAA<br>AGCGAACCTC | C | gap | Pro | Pro<br>(1397) | FRAMESHIFT | struct            | Human Gene SWISSPROT-<br>ID:Q02440 DILUTE MYOSIN HEAVY<br>CHAIN, ISOFORM I (MYOSIN<br>HEAVY CHAIN P190) (MYOSIN-V) -<br>GALLUS GALLUS (CHICKEN), 1829<br>aa.   | 0        | 15<br>(15q21) |
| 1025 | cg43916919 | 1130 | GAAGAAGACGC<br>CCTGGTTCTCTT<br>GC[G/gap]CCACA<br>GGCACCGGCTT<br>CAGCTTCTC | G | gap | Ala | Gly<br>(1398) | FRAMESHIFT | struct            | Human Gene SWISSNEW-ID:P40121<br>MACROPHAGE CAPPING PROTEIN<br>(ACTIN-REGULATORY PROTEIN<br>CAP-G) - HOMO SAPIENS (HUMAN),<br>348 aa.lpcis:SWISSPROT-ID:P40121<br>MACROPHAGE CAPPING PROTEIN<br>(ACTIN-REGULATORY PROTEIN<br>CAP-G) - HOMO SAPIENS (HUMAN),<br>348 aa. | 4.3E-188 | 2 (2cen)      |
| 1026 | cg21428405 | 293  | ATCTCTTCAGGG<br>GCGAGGTTCCG<br>GT[C/gap]GCGCA<br>GCGGAACGCGG<br>TCGAGCTCG | C | gap | Asp | Thr<br>(1399) | FRAMESHIFT | synthase          | Human Gene Similar to SWISSNEW-<br>ID:P54876<br>PHOSPHORIBOSYLFORMYLGLYCI<br>NAMIDINE SYNTHASE II (EC<br>6.3.5.3) (FGAM SYNTHASE II) -<br>MYCOBACTERIUM<br>TUBERCULOSIS, 754 aa.   | 2.2E-56  |               |
| 1027 | cg43336100 | 290  | ATCATGCTGGA<br>GAACTCGCAGA<br>TGA[G/gap]AGAG<br>CGCATGCTGCT<br>GCAAGCCACG | G | gap | Arg | Lys<br>(1400) | FRAMESHIFT | tnf               | Human Gene SWISSPROT-<br>ID:P26022 PENTAXIN-RELATED<br>PROTEIN PTX3 PRECURSOR<br>(TUMOR NECROSIS FACTOR-<br>INDUCIBLE PROTEIN TSG-14) -<br>HOMO SAPIENS (HUMAN), 381 aa.   | 2.2E-207 | 3 (3q25)      |

|      |            |      |   |     |     |               |            |                      |  |            |    |
|------|------------|------|---|-----|-----|---------------|------------|----------------------|--|------------|----|
| 1028 | cg39517655 | 438  | GGGGCCCTTAC<br>TCGCTATGCTG<br>CAA[G/gap]GGC<br>CCCGGGCCTTG<br>GCTTCGGCCGC | G   | gap | Gly<br>(1401) | FRAMESHIFT | transcript<br>factor | Human Gene SWISSPROT-<br>ID:Q14209 TRANSCRIPTION<br>FACTOR E2F2 (E2F-2) - HOMO<br>SAPIENS (HUMAN), 437 aa.   | 1.4E-237   | 1  |
| 1029 | cg43954704 | 1391 | CCCACTGGAAG<br>TGGAGGCTCCA<br>GTC[A/gap]AACC<br>CCCCCTTGAGC<br>TCCGAGGCAG | A   | gap | Phe<br>(1402) | FRAMESHIFT | transferase          | Human Gene Similar to SPTREMBL-<br>ID:Q29121 UDP-<br>GALNAC:POLYPEPTIDE ALFA-1,0<br>N-ACETYLGALACTOSAMINYL<br>TRANSFERASE - SUS SCROFA<br>(PIG), 559 aa.                             | 1.1E-68    | 2  |
| 1030 | cg43986426 | 1227 | GCGGACAGTCG<br>CCCTAAGCAGT<br>GCA[A/gap]GGTG<br>TCTTGAGCCCTA<br>TGGTGGCCA | A   | gap | Gly<br>(1403) | FRAMESHIFT | ubiquitin            | Human Gene SWISSPROT-<br>ID:P41226 UBIQUITIN-ACTIVATING<br>ENZYME E1 HOMOLOG (D8) -<br>HOMO SAPIENS (HUMAN), 1011 aa.  | 0          | 1  |
| 1031 | cg43917221 | 2853 | GAAATGTCATCC<br>ACGGTATTTTT<br>TT[gap]CAGTTT<br>TAGTTTGACCAA<br>AGCTTTA   | T   | gap | Lys<br>(1404) | FRAMESHIFT | UNCLAS<br>SIFIED     | Human Gene SWISSNEW-<br>ACC:Q13563 POLYCYSTIN 2<br>(AUTOSOMAL DOMINANT<br>POLYCYSTIC KIDNEY DISEASE<br>TYPE II PROTEIN) (POLYCYSTWIN)<br>(R48321) - Homo sapiens (Human),<br>968 aa. | 0 4 (4q21) |    |
| 1032 | cg43918356 | 2640 | ATGTCATCTTCA<br>TCTAGAAACGC<br>CC[gap/A]TCACG<br>GAAATGGAATTG<br>CTGCCAGA | gap | A   | Met<br>(1405) | FRAMESHIFT | UNCLAS<br>SIFIED     | Human Gene SPTREMBL-<br>ACC:O75176 KIAA0692 PROTEIN -<br>HOMO SAPIENS (HUMAN), 783 aa<br>(fragment).   | 0          | 12 |
| 1033 | cg43918446 | 2812 | CTTTCCACATG<br>ACTTGTTACATT<br>C[C/gap]GACCAC<br>TGGGACCACTC<br>GGTGAGCT  | C   | gap | Ser<br>(1406) | FRAMESHIFT | UNCLAS<br>SIFIED     | Human Gene SWISSPROT-<br>ACC:P35446 F-SPONDIN<br>PRECURSOR - Rattus norvegicus<br>(Rat), 807 aa.   | 0          |    |



|      |            |      |  |   |     |     |               |            |                  |  |   |          |
|------|------------|------|--|---|-----|-----|---------------|------------|------------------|--|---|----------|
| 1034 | cg43927750 | 2857 | TAAAGTTATTC<br>TCCAATGGTGAT<br>T[G/gap]GGCAAG<br>CCCTGCCTCCT<br>GTATTCTT     | G | gap | Pro | Pro<br>(1407) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:Q13496 MYOTUBULARIN -<br>Homo sapiens (Human), 603 aa.   | 0 | X (Xq28) |
| 1035 | cg43961075 | 1344 | GGGTAGGATTG<br>CTCATTTTCAGGG<br>CA[G/gap]CTGTC<br>GCAAGCATCTC<br>CCACCCCGT   | G | gap | Ser | Ser<br>(1408) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P49746 THROMBOSPONDIN 3<br>PRECURSOR - Homo sapiens<br>(Human), 956 aa.                             | 0 | 1        |
| 1036 | cg43961763 | 1192 | CATCTAGGTCAA<br>CAGGAAGGTCA<br>AG[C/gap]TCCCG<br>CTCCGGTTCCA<br>CTGATCCAT    | C | gap | Glu | Asp<br>(1409) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P13521 SECRETOGRAININ II<br>PRECURSOR (SGII)<br>(CHROMOGRANIN C) - Homo<br>sapiens (Human), 617 aa. | 0 | 2        |
| 1037 | cg43968223 | 2979 | GTTCTGTTCTTG<br>TAGCGCTTTCTG<br>C[G/gap]CTGCAG<br>CATGATCTGAAG<br>CTTGTTG    | G | gap | Arg | Ala<br>(1410) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O60342 KIAA0602 PROTEIN -<br>HOMO SAPIENS (HUMAN), 962 aa<br>(fragment).                             | 0 | 14       |
| 1038 | cg43980727 | 2673 | CCCTCCAGGTA<br>GAGGCCTAGGA<br>AGG[C/gap]CCCA<br>GAACTGAAGCC<br>GAAGCGCTGG    | C | gap | Ala | Pro<br>(1411) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P38432 P80-COILIN - Homo<br>sapiens (Human), 576 aa.  | 0 | 17       |
| 1039 | cg43999667 | 3941 | TTCTGTTTTGTC<br>AGGACTTTTTTT<br>TT[G/gap]CTACAA<br>GTTGTTTTTCTG<br>GGATCAC   | T | gap | Glu | Glu<br>(1412) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O60281 KIAA0530 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1563 aa<br>(fragment).                            | 0 | 6        |
| 1040 | cg44022781 | 3927 | GTATCAAAAGTGC<br>TCTTTCCAACCT<br>TT[G/gap]GGAGGC<br>CCCATCACCACCT<br>ACCGGTA | T | gap | Pro | Pro<br>(1413) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q14692 KIAA0187 PROTEIN -<br>HOMO SAPIENS (HUMAN), 1282 aa.  | 0 |          |

|      |            |      |  |   |     |     |               |            |                  |  |           |    |
|------|------------|------|--|---|-----|-----|---------------|------------|------------------|--|-----------|----|
| 1041 | cg44919370 | 571  | CGTGGACTTTTC<br>CGAGGATGACC<br>CC[C/gap]TGGAG<br>GCCACTGTCCA<br>TTGGGCCCC  | C | gap | Leu | Trp<br>(1414) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O60624 CLASS I CYTOKINE<br>RECEPTOR - HOMO SAPIENS<br>(HUMAN), 636 aa.             | 0         | 19 |
| 1042 | cg44932924 | 2612 | TCTACAACCAGA<br>GCCAGGAATTA<br>CA[G/gap]ACGAA<br>GCTGGAGGACT<br>GCAGGAACA  | G | gap | Thr | Arg<br>(1415) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q92574 HAMARTIN<br>(MYELOBLAST KIAA0243) - HOMO<br>SAPIENS (HUMAN), 1164 aa.       | 0         | 9  |
| 1043 | cg43991434 | 1167 | GGGTGCAAGG<br>GCCTTGGGGAA<br>ATA[G/gap]TCCT<br>GCTGCACCATG<br>TGGTTCAGCG   | G | gap | Asp | Asp<br>(1416) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SWISSNEW-<br>ACC:P46060 RAN-GTPASE<br>ACTIVATING PROTEIN 1 - Homo<br>sapiens (Human), 587 aa.       | 1.7E-304  | 22 |
| 1044 | cg44931278 | 1264 | CCTCCTCCAGG<br>GAAGCACTGGC<br>CAG[G/gap]TCCT<br>GCAGTGTAGGC<br>CACTTCTGCA  | G | gap | Asp | Asp<br>(1417) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q15830 MUTY HOMOLOG -<br>HOMO SAPIENS (HUMAN), 535 aa.                             | 4.5E-280  | 1  |
| 1045 | cg43949042 | 427  | CACAGCTGCGT<br>TGCCATAGTTGC<br>CC[T/gap]GGAAA<br>AAGCGGCCCCAC<br>GAACCAGGC | T | gap | Gln | Arg<br>(1418) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O75907 ACAT RELATED GENE<br>PRODUCT 1 - HOMO SAPIENS<br>(HUMAN), 488 aa.           | 6.10E-268 |    |
| 1046 | cg43972066 | 2313 | TAAATTGACTT<br>TTCTCATGTAAA<br>A[A/gap]TGTCTA<br>ATGCGATGTATT<br>TGGTAAT   | A | gap | His | His<br>(1419) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O60747 PUTATIVE G-BINDING<br>PROTEIN - HOMO SAPIENS<br>(HUMAN), 562 aa (fragment). | 4.10E-221 | 10 |

|      |            |      |   |   |     |     |               |            |                  |   |           |  |
|------|------------|------|---|---|-----|-----|---------------|------------|------------------|---|-----------|--|
| 1047 | cg43955639 | 723  | GGGGGACTGG<br>GGACCTCGTCT<br>GTT[G/gap]GGTT<br>CCCCTCCTCCA<br>GGGTAGCGGC    | G | gap | Pro | Gln<br>(1420) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O15417 CAGL79 - HOMO<br>SAPIENS (HUMAN), 413 aa<br>(fragment).  | 2.80E-215 |  |
| 1048 | cg43955639 | 725  | GGGTACTGGGG<br>ACCTCGTCTGTT<br>GG[G/gap]TTCCC<br>CTCCTCCAGGG<br>TAGCGGCTC   | G | gap | Asn | Asn<br>(1421) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O15417 CAGL79 - HOMO<br>SAPIENS (HUMAN), 413 aa<br>(fragment).  | 2.80E-215 |  |
| 1049 | cg43965656 | 391  | CTGCCTATTCTG<br>AACCAGCCAAC<br>ATT[C/gap]TGAGA<br>TTGTTGCCAATG<br>CCCCGAGGT | C | gap | Ser | Leu<br>(1422) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:Q99541 ADIPOPHILIN - HOMO<br>SAPIENS (HUMAN), 437 aa<br>(fragment).   | 7.20E-210 |  |
| 1050 | cg43944615 | 2370 | TACATGGCACA<br>GAGGAAGAAGC<br>GCA[G/gap]CAC<br>GGCGCTGCAGT<br>TCACGTCCACC   | G | gap | Leu | Cys<br>(1423) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SPTREMBL-<br>ACC:O14877 FRPHE - HOMO<br>SAPIENS (HUMAN), 346 aa.   | 1.30E-192 |  |
| 1051 | cg43323906 | 334  | CTCTGGTGCTG<br>CTCCTCTGAAGA<br>TT[C/gap]AAGCT<br>TATTTCAATGAG<br>ACTGCAGA   | C | gap | Gln | Lys<br>(1424) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P42081 T LYMPHOCYTE<br>ACTIVATION ANTIGEN CD86<br>PRECURSOR (ACTIVATION B7-2<br>ANTIGEN) (CTLA-4 COUNTER-<br>RECEPTOR B7.2) (B70) (FUN-1)<br>(BU63) - Homo sapiens (Human), 329<br>aa. | 1.80E-174 |  |
| 1052 | cg44004690 | 251  | GAGGAGGAGGA<br>GGTGGAGGAGG<br>AGG[A/gap]GGG<br>AGAAAGAGGATG<br>TTTTACCCGAG  | A | gap | Glu | Gly<br>(1425) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAAT4892 KIAA0869 PROTEIN -<br>HOMO SAPIENS (HUMAN), 888 aa<br>(fragment).   | 2.50E-161 |  |

|      |            |     |   |     |     |               |            |                  |   |           |    |
|------|------------|-----|---|-----|-----|---------------|------------|------------------|---|-----------|----|
| 1053 | cg44004690 | 402 | ACCGGAGAGTG<br>GGCACCCCGTC<br>CCA[G/gap]GGG<br>CCATTTCTTCGA<br>GGGAGCACCA | G   | gap | Gly<br>(1426) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA74892 KIAA0869 PROTEIN -<br>HOMO SAPIENS (HUMAN), 888 aa<br>(fragment).   | 2.50E-161 |    |
| 1054 | cg43957283 | 322 | TCGAGGGTGAC<br>CACAGCCCCAG<br>AGG[G/gap]CCG<br>CAGCACAGCGC<br>AGGGGGTGGCG | G   | gap | Pro<br>(1427) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD27734 CGI-25 PROTEIN -<br>HOMO SAPIENS (HUMAN), 301 aa.   | 1.40E-160 |    |
| 1055 | cg43329741 | 336 | GCTCTACCTGG<br>GCTACACCCCG<br>CAG[G/gap]CGG<br>CCCGTGAAGTG<br>CGCATCATGCA | G   | gap | Ala<br>(1428) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD39906 FH1/FH2 DOMAIN-<br>CONTAINING PROTEIN FHOS -<br>HOMO SAPIENS (HUMAN), 1164 aa.  | 6.70E-159 |    |
| 1056 | cg44010310 | 501 | TTTGTTGAGATG<br>CATGAATTTTT<br>T[gap/T]CTCTATT<br>GCTGCTTGAAAA<br>TTTACA  | gap | T   | Lys<br>(1429) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:BAA32101 BCAP - HOMO<br>SAPIENS (HUMAN), 331 aa.   | 1.30E-155 | 13 |
| 1057 | cg39729127 | 981 | GCTCTCTCTTT<br>ATTGGTAACCAG<br>T[gap/T]GGTGGC<br>CACGAGTCATA<br>CAGGGAAA  | gap | T   | Val<br>(1430) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene TREMBLNEW-<br>ACC:AAD42876 NY-REN-45<br>ANTIGEN - HOMO SAPIENS<br>(HUMAN), 815 aa.   | 3.00E-152 | 1  |
| 1058 | cg43135797 | 861 | AGATCTGTCTCC<br>CCGGAGACCCG<br>GA[G/gap]CCGCT<br>GGCCATTGCAG<br>AAGGCGCCC | G   | gap | Ser<br>(1431) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSPROT-ACC:O14732 MYO-<br>INOSITOL-1(OR 4)-<br>MONOPHOSPHATASE 2 (EC<br>3.1.3.25) (IMP 2) (INOSITOL<br>MONOPHOSPHATASE 2) (MYO-<br>INOSITOL MONOPHOSPHATASE<br>A2) - Homo sapiens (Human), 288 aa. | 1.60E-150 | 18 |

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| 1059 | cg43965796 | 1704 | ATCACTGTTGAT<br>GCTCTGGGCCA<br>CG[C/gap]CAGG<br>GTACTGGATCTT<br>CATGGCCAC   | C | gap | Gly | Ala<br>(1432) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSPROT-ACC:Q60936<br>HYPOTHETICAL HEART PROTEIN -<br>Mus musculus (Mouse), 298 aa<br>(fragment). | 9.00E-148 | 1 |
| 1060 | cg43965796 | 1705 | TCACTGTTGATG<br>CTCTGGGCCAC<br>GC[C/gap]AGGG<br>TACTGGATCTTC<br>ATGGCCACC   | C | gap | Gly | Ala<br>(1433) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSPROT-ACC:Q60936<br>HYPOTHETICAL HEART PROTEIN -<br>Mus musculus (Mouse), 298 aa<br>(fragment). | 9.00E-148 | 1 |
| 1061 | cg42907867 | 1100 | AGGGCCACGGG<br>GTGGGCCAGGG<br>GGC[C/gap]GGG<br>CCATTCCAGTG<br>GCTCCTTGTC    | C | gap | Arg | Arg<br>(1434) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q99769<br>HYPOTHETICAL 26.4 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 255 aa.              | 1.10E-140 | 1 |
| 1062 | cg43922710 | 126  | TCTACCCAGCTA<br>AATACACATTAT<br>G[G/gap]CATTTA<br>GCAAACTAACTT<br>ACAAGTC   | G | gap | Ala | His<br>(1435) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:BAA74897<br>KIAA0874 PROTEIN - HOMO<br>SAPIENS (HUMAN), 601 aa<br>(fragment).         | 4.90E-140 |   |
| 1063 | cg43303845 | 1073 | GCAGGAACGCC<br>TGGATCGGGAG<br>AGG[C/gap]AAGA<br>AAGACAAGAAC<br>GAGAGAGGCT   | C | gap | Gln | Lys<br>(1436) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O93263 AVENA -<br>GALLUS GALLUS (CHICKEN), 550<br>aa.                                  | 1.90E-138 |   |
| 1064 | cg43973762 | 430  | ATAACAGAAAAGC<br>AAGAGAAAGTG<br>GA[G/gap]AACTC<br>TGAAAGAAAGAA<br>GTTCAAAAG | G | gap | Arg | Lys<br>(1437) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:O14777<br>RETINOBLASTOMA-ASSOCIATED<br>PROTEIN HEC - HOMO SAPIENS<br>(HUMAN), 642 aa.  | 2.20E-137 |   |

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| 1065 | cg43918679 | 411  | TCACAGATATCT<br>CCATTGCCAG<br>GA[G/gap]ATGCC<br>CAGCCTGGAGG<br>TGATCACGC  | G   | gap | Met | Cys<br>(1438) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSPROT-ACC:O43822 28.3 KD<br>PROTEIN C21ORF2 (C21ORF-<br>HUMF09G8.5) (YF5/A2) - Homo<br>sapiens (Human), 256 aa. | 3.00E-131 | 21 |
| 1066 | cg38059286 | 503  | GCCGCTCCCTC<br>TTCTCACTGAAG<br>CA[G/gap]ATCTT<br>CCAGGAGGACA<br>AAGACCTGG | G   | gap | Ile | Ser<br>(1439) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAD39906<br>FH1/FH2 DOMAIN-CONTAINING<br>PROTEIN FHOS - HOMO SAPIENS<br>(HUMAN), 1164 aa.             | 4.00E-129 |    |
| 1067 | cg42549778 | 1014 | ACTGTCACCTTC<br>CTGCTGCAGGG<br>CA[G/gap]CCCCC<br>ACCTGTGAGTG<br>GCTCGAGCC | G   | gap | Ser | Thr<br>(1440) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAD29690<br>PUTATIVE ZINC FINGER<br>TRANSCRIPTION FACTOR OVO1 -<br>MUS MUSCULUS (MOUSE), 267 aa.      | 3.70E-126 |    |
| 1068 | cg44921277 | 516  | CCCTGATCATCC<br>TCATCGTGGAG<br>CT[G/gap]TGCGG<br>GCTCCAGGCC<br>GCTTCCCCC  | G   | gap | Cys | Ala<br>(1441) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSPROT-ACC:O35682<br>MYELOID UPREGULATED PROTEIN<br>- Mus musculus (Mouse), 296 aa.                              | 1.70E-120 |    |
| 1069 | cg44921277 | 518  | CTGATCATCCTC<br>ATCGTGGAGCT<br>GT[G/gap]CGGG<br>CTCCAGGCCCG<br>CTTCCCCCTG | G   | gap | Cys | Ser<br>(1442) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SWISSPROT-ACC:O35682<br>MYELOID UPREGULATED PROTEIN<br>- Mus musculus (Mouse), 296 aa.                              | 1.70E-120 |    |
| 1070 | cg42530218 | 327  | GATTTAATACAC<br>AGCAGCAGCAG<br>CA[gap/G]AACTA<br>CATTAGGTGGT<br>CTCTTCAGT | gap | G   | Gln | Gln<br>(1443) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:P70582<br>NUCLEOPORIN P54 - RATTUS<br>NORVEGICUS (RAT), 510 aa.  | 2.00E-118 |    |

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| 1071 | cg42530218 | 329 | ATTAAATACACA<br>GCAGCAGCAGC<br>AA[A/gap]CTACA<br>TTAGGTGGTCTC<br>TTCAGTCA  | A   | gap | Thr | Leu<br>(1444) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:P70582<br>NUCLEOPORIN P54 - RATTUS<br>NORVEGICUS (RAT), 510 aa.                        | 2.00E-118 |    |
| 1072 | cg43325007 | 979 | AGGATACCCCC<br>GAGGAAGGCCG<br>CCA[G/gap]GAAT<br>GCGTGTGCTGG<br>GTAGGTCTTG  | G   | gap | Leu | Trp<br>(1445) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:AAD43195<br>PEROXISOMAL MEMBRANE<br>PROTEIN PMP 24 - HOMO SAPIENS<br>(HUMAN), 212 aa. | 4.80E-110 | 20 |
| 1073 | cg43981269 | 776 | GGCCTACGGCG<br>CCTACGCTCAG<br>GCA[C/gap]TGAT<br>GCAGCAGCAAG<br>CGGCCCTGAT  | C   | gap | Leu | End<br>(1446) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>SPTREMBL-ACC:Q91579<br>RIBONUCLEOPROTEIN - XENOPUS<br>LAEVIS (AFRICAN CLAWED FROG),<br>462 aa.      | 4.50E-105 |    |
| 1074 | cg43250166 | 166 | AGGTGGCCCTC<br>ACACCCAGTGC<br>TGT[G/gap]CTGC<br>GCGGAGGGCTG<br>TACTGAAGGT  | G   | gap | Ala | Asp<br>(1447) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Homologous to<br>TREMBLNEW-ACC:CAB43382<br>HYPOTHETICAL 146.2 KD PROTEIN<br>- HOMO SAPIENS (HUMAN), 1296<br>aa.      | 3.30E-102 | 2  |
| 1075 | cg43982164 | 778 | CTGCGGCGGGT<br>GCTCATCCTGG<br>ACA[gap]C/ATTC<br>ACCTGCCTCCTA<br>TGCTCTTCCA | gap | C   | Asn | Thr<br>(1448) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O15194 HYA22 - HOMO<br>SAPIENS (HUMAN), 340 aa.  | 1.00E-90  |    |
| 1076 | cg43980889 | 812 | TTAAATATAGAC<br>AAGTGGACCAT<br>TTT/gap/GCCTCA<br>AATTCACAGGA<br>GCCAGCAT   | T   | gap | Ala | Pro<br>(1449) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O00581 HYPOTHETICAL 20.5<br>KD PROTEIN - HOMO SAPIENS<br>(HUMAN), 176 aa.                | 4.50E-89  |    |

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| 1077 | cg43970119 | 832 | GTGGCCATTGG<br>TGAGACATCCAT<br>CA[A/gap]TATTG<br>CAAACCAAAAGT<br>TTTATTTTC | A | gap | Ile | Met<br>(1450) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:O88719 CMP-N-<br>ACETYLNEURAMINIC ACID<br>SYNTHETASE (EC 2.7.7.43)<br>(ACYLNEURAMINATE<br>CYTIDYLTRANSFERASE) (CMP-<br>SIALATE PYROPHOSPHORYLASE)<br>(CMP-SIALATE SYNTHASE) - MUS<br>MUSCULUS (MOUSE), 432 aa. | 1.00E-82 | 12 |
| 1078 | cg44030987 | 447 | TCGGCATGTTG<br>AGTGGAACAGT<br>TGT[A/gap]TTTA<br>CTTGAATTCCTCA<br>TCTCCTTCT | A | gap | Tyr | Thr<br>(1451) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA76495 TYPE<br>II MEMBRANE PROTEIN SIMILAR<br>TO CD69 - HOMO SAPIENS<br>(HUMAN), 149 aa.   | 1.90E-81 |    |
| 1079 | cg43320682 | 665 | GGTGGCTCAGG<br>GGCTGGGGGAG<br>GCT[C/gap]CCCT<br>GGGGCTTCAGA<br>CAGCACATAG  | C | gap | Glu | Ser<br>(1452) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB45773<br>HYPOTHETICAL 18.0 KD PROTEIN -<br>HOMO SAPIENS (HUMAN), 162 aa<br>(fragment).  | 6.60E-81 |    |
| 1080 | cg25255686 | 366 | AAGGCACCATC<br>AAGTCGGCGGT<br>GGC[C/gap]TTCG<br>GGCATCTCCTT<br>GCCGAGGGTA  | C | gap | Phe | Ser<br>(1453) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB39700<br>CONSERVED HYPOTHETICAL<br>PROTEIN - STREPTOMYCES<br>COELICOLOR, 384 aa.  | 2.10E-77 |    |
| 1081 | cg43988975 | 371 | CTCCTCCTGAC<br>CGAGTGGGCCG<br>GCA[G/gap]GAG<br>CTTGAAATCGTC<br>ATTGGAGATG  | G | gap | Glu | Ser<br>(1454) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:P50606 MAGO NASHI<br>PROTEIN HOMOLOG - Homo<br>sapiens (Human), and Mus musculus<br>(Mouse), 146 aa.   | 8.00E-76 |    |
| 1082 | cg39523553 | 670 | CACTGGTATGC<br>ACGGCGCGGTC<br>TCC[G/gap]CAGT<br>GTGAGGTCTGC<br>CCGATCCGGG  | G | gap | Gln | Ser<br>(1455) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB40855<br>PUTATIVE ADENINE<br>GLYCOSYLASE - STREPTOMYCES<br>COELICOLOR, 308 aa.  | 7.20E-75 |    |



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| 1083 | cg43951096 | 2953 | CTCCCTCCTGG<br>GTATCTGCATCT<br>TC[gap]/AJAAAAT<br>CTCCTTCTTGGT<br>TTTCATCC | gap | A   | Glu           | End<br>(1456) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q23382 ZK1058.4 -<br>CAENORHABDITIS ELEGANS, 442<br>aa.   | 2.00E-71 | 17 |
| 1084 | cg42831353 | 806  | GGACACAGGCT<br>GCGGTGTAAGC<br>CCG[C/gap]GTCA<br>CCGCCGGCACC<br>TGCAGGAACT  | C   | gap | Thr<br>(1457) | Thr<br>(1457) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD37863<br>PUTATIVE NADH<br>OXIDOREDUCTASE COMPLEX I<br>SUBUNIT - CAENORHABDITIS<br>ELEGANS, 237 aa.                               | 1.30E-67 | 22 |
| 1085 | cg44938009 | 688  | AATACTCCGTGC<br>AGCGAGTGCGT<br>CA[G/gap]CTCCG<br>TGAAGAATTGTA<br>TCAAGGTC  | G   | gap | Leu           | Ser<br>(1458) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SWISSNEW-<br>ACC:O43182 RHO-GTPASE-<br>ACTIVATING PROTEIN 6 (RHO-<br>TYPE GTPASE-ACTIVATING<br>PROTEIN RHOGAPX-1) - Homo<br>sapiens (Human), 587 aa. | 5.80E-66 | X  |
| 1086 | cg43054992 | 315  | CAAAATCACAGC<br>TGAAGAAATGTA<br>T[G/gap]ATATAT<br>TTGGGAAATATG<br>GACCTAT  | G   | gap | Asp           | Ile<br>(1459) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:AAD34105 CGI-<br>110 PROTEIN - HOMO SAPIENS<br>(HUMAN), 125 aa.   | 4.60E-64 | 2  |
| 1087 | cg39516123 | 928  | CCTGGGGCTCA<br>CCAAGGCAACC<br>TGG[C/gap]CTCC<br>GGTCTTCATAGC<br>AATGCAATA  | C   | gap | Ala           | Ala<br>(1460) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q04205 TENSIN - Gallus gallus<br>(Chicken), 1744 aa.   | 5.10E-62 |    |
| 1088 | cg43983590 | 713  | GGAGGAGCCAG<br>GCGAGCACACC<br>CCC[C/gap]TGTT<br>GGCCCCTGCCA<br>CGGCCAGGCC  | C   | gap | Leu           | Cys<br>(1461) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SPTREMBL-<br>ACC:Q19498 SIMILAR TO<br>MELIBIOSE CARRIER PROTEIN -<br>CAENORHABDITIS ELEGANS, 501<br>aa.  | 1.50E-60 |    |

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|------|------------|-----|---|---|-----|-----|---------------|------------|------------------|---|----------|----|
| 1089 | cg44128084 | 499 | CGCGGGCGCAT<br>GCTCGACGTTT<br>TGG[C/gap]GTCT<br>GTCGACGAGTT<br>GCCGGTGCAA | C | gap | Ala | Gly<br>(1462) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SP TREMBL-<br>ACC:O33196 HYPOTHETICAL 32.9<br>KD PROTEIN - MYCOBACTERIUM<br>TUBERCULOSIS, 307 aa.                                 | 1.70E-59 |    |
| 1090 | cg44128084 | 524 | CGTCTGTCGAC<br>GAGTTGCCGGT<br>GCA[A/gap]CGCT<br>GGAGCTGCGAC<br>GGGATCCTGG | A | gap | Arg | Ala<br>(1463) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SP TREMBL-<br>ACC:O33196 HYPOTHETICAL 32.9<br>KD PROTEIN - MYCOBACTERIUM<br>TUBERCULOSIS, 307 aa.                                 | 1.70E-59 |    |
| 1091 | cg43976473 | 931 | GGCCCTGTGCT<br>TGGAGCCGTGG<br>GCT[C/gap]CGTA<br>GCCCGAGTGAT<br>AAGCCATGGC | C | gap | Gly | Glu<br>(1464) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SP TREMBL-<br>ACC:O35946 HYPOTHETICAL 14.9<br>KD PROTEIN - RATTUS<br>NORVEGICUS (RAT), 137 aa.                                    | 3.50E-59 | 11 |
| 1092 | cg40309770 | 385 | TTCCGGCCGCC<br>GCGTCCAGGGC<br>TCG[C/gap]CCGC<br>TGAGGTCGTTT<br>ATGACCCCGC | C | gap | Gly | Gly<br>(1465) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to SWISSPROT-<br>ACC:Q60870 POLYPOSIS LOCUS<br>PROTEIN 1 HOMOLOG (TB2<br>PROTEIN HOMOLOG) (GP106) -<br>Mus musculus (Mouse), 185 aa. | 4.10E-56 |    |
| 1093 | cg42725664 | 184 | AGATAGCTGAG<br>AATATTCTGCGC<br>AA[G/gap]CCTCA<br>CAGCTTGTTTCC<br>TGCGAGCC | G | gap | Leu | Leu<br>(1466) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:BAA74896<br>KIAA0873 PROTEIN - HOMO<br>SAPIENS (HUMAN), 466 aa<br>(fragment).                                    | 1.5E-51  |    |
| 1094 | cg39380052 | 497 | ATGAGATCGAC<br>GCCTTGCGCGG<br>CCG[C/gap]GGC<br>GTAGACATTCC<br>GCACCCGCTCA | C | gap | Gly | Ala<br>(1467) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene Similar to<br>TREMBLNEW-ACC:CAB42016<br>PUTATIVE ADENYLOSUCINATE<br>SYNTHETASE - STREPTOMYCES<br>COELICOLOR, 427 aa.                         | 1.3E-50  |    |

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| 1095 | cg44928804 | 1181 | CTCTCAATCATG<br>CCGCTTTAGAG<br>AA[T/gap]GCAAC<br>ATGGGCAACCT<br>GATTGTGA | T | gap | Cys | Ala<br>(1468) | FRAMESHIFT | UNCLAS<br>SIFIED | Human Gene SWISSPROT-<br>ACC:P21589 5'-NUCLEOTIDASE<br>PRECURSOR (EC 3.1.3.5) (ECTO-<br>NUCLEOTIDASE) (5'-NT) (CD73<br>ANTIGEN) - Homo sapiens (Human),<br>574 aa. | 9.1e-313 | 6 (6q14) |
|------|------------|------|--|---|-----|-----|---------------|------------|------------------|--|----------|----------|

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- ☒ I hereby claim the benefit under Title 35, United States Code, § 119(e) or §120 of any United States application(s), or §365(c) of any PCT International application(s) designating the United States of America listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose material information as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

| <b>Application No.</b><br><i>(U.S.S.N.)</i> | <b>Filing Date</b><br><i>(dd/mm/yy)</i> | <b>Status</b><br><i>(Patented, Pending, Abandoned)</i> |
|---|---|--|
| 60/167,383                                  | November 24, 1999                       | Pending  |

PCT International Applications designative the United States:

| <b>PCT Appln No.</b> | <b>US Serial No.</b> | <b>PCT Filing Date</b> | <b>Status</b> |
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|                      |                      |                        |               |

I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith:

| <b>Attorney or Agent</b> | <b>Registration No.</b> | <b>Attorney or Agent</b> | <b>Registration No.</b> |
|--------------------------|-------------------------|--------------------------|-------------------------|
| Kevin Ainsworth          | 39,586                  | Kristin E. Konzak        | 44,848                  |
| Ingrid Beattie           | 42,306                  | Cynthia Kozakiewicz      | 42,764                  |
| David B. Bernstein       | 32,112                  | Barry Marenberg          | 40,715                  |
| Naomi Biswas             | 38,384                  | William Marino           | 44,219                  |
| David F. Crosby          | 36,400                  | Robert Klauzinski        | 42,742                  |
| James G. Cullem          | 43,569                  | A. Jason Mirabito        | 28,161                  |
| Brett N. Dorny           | 35,860                  | Michel Morency           | Limited Recognition     |
| Marianne Downing         | 42,870                  | Bradley Olson            | 40,750                  |
| Ivor R. Elrifi           | 39,529                  | Carol H. Peters          | 45,010                  |
| Heidi A. Erlacher        | 45,409                  | Michael Renaud           | 44,299                  |
| Christina Gadiano        | 37,628                  | Brian Rosenbloom         | 41,276                  |
| John A. Harre            | 37,345                  | Thomas M. Sullivan       | 39,392                  |
| Shane Hunter             | 41,858                  | Howard Susser            | 33,556                  |
| David E. Johnson         | 41,874                  | Shelby J. Walker         | 45,192                  |
| Kris Kalidindi           | 41,461                  | Martin M. Zoltick        | 35,745                  |
| Christina Karnakis       | 45,899                  |                          |                         |

Address all telephone calls to Ivor R. Elrifi at telephone number 617/348-1747.

Address all correspondence to:

Ivor R. Elrifi, Ph.D.  
Mintz, Levin, Cohn, Ferris, Glovsky and Popeo, P.C.  
One Financial Center  
Boston, Massachusetts 02111

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or patent issued thereon.

\_\_\_\_\_  
Inventor's Signature  
Full Name of Inventor: Richard A. Shimkets, Ph.D.  
Citizenship: USA  
Residence: USA  
Post Office Address: West Haven, CT 06516

\_\_\_\_\_  
Date

\_\_\_\_\_  
Inventor's Signature  
Full Name of Inventor: Martin Leach  
Citizenship: USA  
Residence: USA  
Post Office Address: Webster, MA 01570

\_\_\_\_\_  
Date

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51

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42

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00748334 110000



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<210> 166  
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| Variable            | Mean | SD   | Min | Max  | Median | Mode | Skewness | Kurtosis | Shapiro-Wilk | Normality |
|---------------------|------|------|-----|------|--------|------|----------|----------|--------------|-----------|
| Age                 | 35.2 | 12.5 | 18  | 65   | 32     | 30   | 0.15     | 2.10     | 0.98         | Normal    |
| Gender              | 1.2  | 0.4  | 1   | 2    | 1      | 1    | 0.05     | 0.10     | 0.99         | Normal    |
| Marital Status      | 2.1  | 0.8  | 1   | 3    | 2      | 2    | 0.10     | 0.50     | 0.97         | Normal    |
| Education           | 15.8 | 2.5  | 10  | 20   | 16     | 16   | 0.08     | 0.30     | 0.99         | Normal    |
| Income              | 1200 | 300  | 500 | 2000 | 1100   | 1000 | 0.12     | 0.80     | 0.96         | Normal    |
| Occupation          | 1.5  | 0.5  | 1   | 3    | 1      | 1    | 0.05     | 0.10     | 0.99         | Normal    |
| Health Status       | 2.5  | 0.5  | 1   | 3    | 2      | 2    | 0.05     | 0.10     | 0.99         | Normal    |
| Stress Level        | 3.2  | 1.0  | 1   | 5    | 3      | 3    | 0.10     | 0.50     | 0.97         | Normal    |
| Life Satisfaction   | 4.5  | 0.8  | 3   | 5    | 4      | 4    | 0.05     | 0.10     | 0.99         | Normal    |
| Resilience          | 3.8  | 0.9  | 2   | 5    | 3      | 3    | 0.10     | 0.50     | 0.97         | Normal    |
| Optimism            | 4.2  | 0.7  | 3   | 5    | 4      | 4    | 0.05     | 0.10     | 0.99         | Normal    |
| Emotional Stability | 3.5  | 0.6  | 2   | 4    | 3      | 3    | 0.05     | 0.10     | 0.99         | Normal    |
| Self-Esteem         | 4.0  | 0.8  | 3   | 5    | 4      | 4    | 0.05     | 0.10     | 0.99         | Normal    |
| Life Satisfaction   | 4.5  | 0.8  | 3   | 5    | 4      | 4    | 0.05     | 0.10     | 0.99         | Normal    |
| Resilience          | 3.8  | 0.9  | 2   | 5    | 3      | 3    | 0.10     | 0.50     | 0.97         | Normal    |
| Optimism            | 4.2  | 0.7  | 3   | 5    | 4      | 4    | 0.05     | 0.10     | 0.99         | Normal    |
| Emotional Stability | 3.5  | 0.6  | 2   | 4    | 3      | 3    | 0.05     | 0.10     | 0.99         | Normal    |
| Self-Esteem         | 4.0  | 0.8  | 3   | 5    | 4      | 4    | 0.05     | 0.10     | 0.99         | Normal    |

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09710334 13250

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CG43258867  
CG42907867  
CG43920176

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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43992566

<400> 248  
atttaaattct gaagcagaaa aaaaagacaa ttacaaaga attattgagc

50

<210> 249  
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<212> DNA  
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<223> single nucleotide polymorphism

<221> misc\_feature  
<222> (0)...(0)  
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tccctgcacg cctttacgtc agactatcac cacaagagcc ttgagtgtcc a

51

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<222> (26)...(0)  
<223> single nucleotide polymorphism

<221> misc\_feature  
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<400> 250  
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51

<210> 251  
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<400> 251  
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51

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 aactgcagac aaattttcaa attcaattct ttacttctcc aagatcttcg a 51  
  
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 <223> Accession number cg43976566  
  
 <400> 253  
 ctttaatgaa acacttttga tcgtcgggtgc tgaagtgaaa agaattgtgct g 51  
  
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 <221> misc\_feature  
 <222> (0)...(0)  
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 <400> 254  
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 <222> (0)...(0)  
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<400> 255  
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<210> 256  
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<400> 256  
agtggcccct ttcccgccct gaagacgttt cacacgaaaa ggcggtttgt t 51

<210> 257  
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<400> 257  
tggcaaaact gccagcagcg gttgctgaaa atgctgggtt cggcgcctac t 51

<210> 258  
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<400> 258  
accagctcgg agagggcact tgagatggtc tatgaacaaa tctgtctaaa a 51

<210> 259  
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51

<210> 260  
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<400> 260  
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51

<210> 261  
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<400> 261  
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51

<210> 262  
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<400> 265  
caggagtaga tgaggcctgg cacacgtagc agaaggtaat ggttctatag g 51

<210> 266  
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<400> 266  
atgaggcctg gcacacatag cagaaagtaa tggttctata ggtgtatctt c 51

<210> 267  
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<223> Accession number cg43977021

<400> 267  
taatgcactt tgggctagag aaatacaaaa atcacacgta acaaaaacaa a 51

<210> 268  
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<223> single nucleotide polymorphism

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<223> Accession number cg43999373

<400> 268  
cacagaattc agaacttttt caccgccgaac tggagaagga gcactccgtc a 51

<210> 269  
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<212> DNA

<213> Homo sapiens

<220>

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<222> (26)...(0)

<223> single nucleotide polymorphism

<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg43980889

<400> 269

tttgagagct gcagcagaag cggctttatc acagactgga tttagttatg a

51

<210> 270

<211> 51

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ggctgtatca cagactggat ttagtgatga tgaaaatact ggactgtatt t

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<221> misc\_feature

<222> (0)...(0)

<223> Accession number cg44030196

<400> 271

tagattgttc agtactcagc tcacccccat aagaccattt ctctctgcg

50

<210> 272

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<212> DNA

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002274 123760

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<400> 272  
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51

<210> 273  
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<400> 273  
agaagacagc gcgcagaaat agtgcagaga gaaatgacca gtactattta t

51

<210> 274  
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<400> 274  
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51

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CG40336929

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50

<210> 276  
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50

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gggaagtaaa atgaaggaag cagacttctt gtcacatcttt ccaaataaaa t

51

<210> 278  
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<400> 278  
taaggccaga gcttggtgtgc tgggccagaa atcacctgct gcattcctgtg

50

<210> 279  
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<400> 279  
cagtgatgtg ctggcccttt cagggccaca ggccccttca gcttcaccgg a

51

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ccaaactatc tcaccctacc ctcccagga tccacttctt tggaatgaca a

51

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<223> single nucleotide polymorphism

<221> misc\_feature

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<223> Nucleotide deleted between bases 25 and 26

<221> misc\_feature  
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ctattttatc catccatggt ctcccaatct gtgctttott tcaacagggt

50

<210> 282  
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<213> Homo sapiens

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<223> Accession number cg35060315

<400> 282  
ttttatccat ccatgttctc ccaaaaatctg tgctttcttt caacagggtta t

51

<210> 283  
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<212> DNA  
<213> Homo sapiens

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<400> 283  
gttctcccaa atctgtgctt tcttttaaca gggttatatat taaaactatt t

51

<210> 284  
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<223> Accession number cg35060315



<400> 284  
cccaaactctg tgctttcttt caacacgtta tatattaaaa ctatttcatg a

51

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<223> Accession number cg44126579

<400> 285  
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42

<210> 286  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43951096

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cctctctctcc aagagttggt tccgcagagg tggaaagaac tctcaatagt

50

<210> 287  
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<400> 287  
cacagccata atatagagaa cagagttctc catgaacatc caccaggctg 50

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<400> 288  
agcagccagc ttcatgtggt gcaaatgcct ctctcaggtg agtcaaagga g 51

<210> 289  
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<400> 289  
tcacctcaga tgagtgtggc tccccgcgt cccatactgc agcctgcccc t 51

<210> 290  
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CG43951096

<221> misc\_feature  
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aagggaagcc tatkctatatt ttttttcctt tgcgaaaaca gaagccaagt 50

<210> 291  
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<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43969533

<400> 291  
agggaagcct atcctatattt tttttccttt gcgaaaacag aagccaagtt 50

<210> 292  
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<212> DNA  
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<222> (0)...(0)  
<223> Accession number cg39376027

<400> 292  
ccggggaggt ggttctggta atctgtgggg gagccgggac aggcgccccg a 51

<210> 293  
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CG39376027

[illegible]

<400> 293

51

<211> 51

<213> Homo sapiens

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<400> 294

51

<211> 51

<213> Homo sapiens

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<400> 295

51

<211> 51

<213> Homo sapiens

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$$\langle 222 \rangle \quad (0) \dots (0)$$

<400> 296

51

<210> 297  
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51

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<400> 298  
ttgttgtag caagcttttc gcctatatt tagactaacc ctgcttatt c

51

<210> 299  
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<223> Accession number cg43085556

<400> 299  
ttttcgcta catttagac taaccttgct tattcctgtg aatcaagtgg t

51

<210> 300  
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<223> single nucleotide polymorphism

<221> misc\_feature  
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<223> Accession number cg43085556

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taaccctgct tattcctgtg aatcacgtgg tgatcttctg cagcttgga t

51

<210> 301  
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<220>  
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<223> single nucleotide polymorphism

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg43920089

<400> 301  
gcatttgctg cttgtgcttg attttatttg gctcaatccc ttctggcag c

51

<210> 302  
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<223> single nucleotide polymorphism

<221> misc\_feature  
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<222> (0)...(0)  
<223> Accession number cg43950850

<400> 302  
aaacatgttc catcaaattc agaaaagcag gtatcagtga aactggagca

50

<210> 303  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
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[illegible] $\langle 222 \rangle \quad (0) \dots (0)$ 

<400> 303

51

<211> 51

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<222> (26) ... (0)

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<223> Accession number cg44128084

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51

<210> 305

<211> 51

<212> DNA

<213> Homo sapiens

<221> allele

 $\langle 222 \rangle \quad (26) \dots (0)$ 

<223> single nucleotide polymorphism

$$\langle 222 \rangle \quad (0) \dots (0)$$

<223> Accession number cg43976473

gacgctcgct gtecccgagg gcccgctgcg ccgcctcgtg ggtacgaata c

51

<210> 306

<211> 51

<212> DNA

<213> Homo sapiens

<221> allele

 $\langle 222 \rangle \quad (26) \dots (0)$ 

<223> single nucleotide polymorphism

 $\langle 222 \rangle \quad (0) \dots (0)$ 

<223> Accession number cg44924858

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<210> 307  
<211> 51  
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<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> single nucleotide polymorphism

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924858

<400> 307  
cgttactttc accgtgctg ctgttccac aggaagagtc tgtctgttcc a 51

<210> 308  
<211> 51  
<212> DNA  
<213> Homo sapiens

<220>  
<221> allele  
<222> (26)...(0)  
<223> single nucleotide polymorphism

<221> misc\_feature  
<222> (0)...(0)  
<223> Accession number cg44924858

<400> 308  
accccagctt gcccggcagc acacagaact gtttcttttg cttgacgaat a 51

<210> 309  
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<212> DNA  
<213> Homo sapiens

<220>  
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<222> (26)...(0)  
<223> single nucleotide polymorphism

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<223> Accession number cg43961591

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<210> 310  
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<213> Homo sapiens

<220>

<221> allele

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<223> Nucleotide deleted between bases 25 and 26

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09710331 116000

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CG43312829

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tcattttctc ctcaaaagga gtgatcttgc caatgcctag gttcttctcc a

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51

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<223> Accession number cg43297806

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51

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CG41616031

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51

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CG44005525

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51

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51

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51

<210> 488

<211> 51

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51

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CG43970200





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51

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51

<210> 505  
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51

<210> 506  
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51

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CG44020180



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| Variable                 | Mean | SD   | Min | Max |
|--------------------------|------|------|-----|-----|
| Age                      | 34.5 | 10.2 | 18  | 65  |
| Gender                   | 1.2  | 0.4  | 0   | 2   |
| Marital status           | 1.5  | 0.5  | 0   | 3   |
| Education                | 12.5 | 1.5  | 9   | 16  |
| Income                   | 15.2 | 3.8  | 10  | 25  |
| Occupation               | 1.8  | 0.8  | 0   | 4   |
| Health status            | 1.2  | 0.4  | 0   | 2   |
| Stress level             | 2.5  | 1.2  | 1   | 4   |
| Life satisfaction        | 3.8  | 1.5  | 2   | 5   |
| Resilience               | 4.2  | 1.8  | 2   | 6   |
| Optimism                 | 3.5  | 1.2  | 2   | 5   |
| Gratitude                | 4.0  | 1.5  | 2   | 6   |
| Self-esteem              | 3.2  | 1.0  | 2   | 5   |
| Empathy                  | 3.8  | 1.2  | 2   | 5   |
| Prosocial behavior       | 3.5  | 1.0  | 2   | 5   |
| Life purpose             | 4.5  | 1.5  | 2   | 6   |
| Meaning in life          | 4.0  | 1.2  | 2   | 6   |
| Existential well-being   | 4.2  | 1.5  | 2   | 6   |
| Psychological well-being | 4.5  | 1.8  | 2   | 6   |
| Overall well-being       | 4.0  | 1.5  | 2   | 6   |

| Variable           | Mean | SD   | Min | Max |
|--------------------|------|------|-----|-----|
| Age                | 34.5 | 10.2 | 18  | 65  |
| Gender             | 1.2  | 0.4  | 0   | 2   |
| Marital status     | 1.5  | 0.5  | 0   | 3   |
| Education          | 12.5 | 1.5  | 9   | 16  |
| Income             | 15.2 | 3.8  | 10  | 25  |
| Occupation         | 1.8  | 0.8  | 0   | 4   |
| Health status      | 1.1  | 0.3  | 0   | 2   |
| Stress level       | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction  | 3.2  | 1.5  | 1   | 5   |
| Resilience         | 2.8  | 1.1  | 1   | 5   |
| Optimism           | 3.5  | 1.3  | 1   | 5   |
| Gratitude          | 3.8  | 1.4  | 1   | 5   |
| Self-efficacy      | 3.1  | 1.2  | 1   | 5   |
| Hope               | 3.4  | 1.3  | 1   | 5   |
| Forgiveness        | 3.6  | 1.4  | 1   | 5   |
| Empathy            | 3.3  | 1.2  | 1   | 5   |
| Compassion         | 3.7  | 1.5  | 1   | 5   |
| Kindness           | 3.9  | 1.6  | 1   | 5   |
| Generosity         | 3.5  | 1.4  | 1   | 5   |
| Patience           | 3.2  | 1.3  | 1   | 5   |
| Humility           | 3.4  | 1.4  | 1   | 5   |
| Modesty            | 3.6  | 1.5  | 1   | 5   |
| Meekness           | 3.8  | 1.6  | 1   | 5   |
| Gentleness         | 3.5  | 1.4  | 1   | 5   |
| Mildness           | 3.7  | 1.5  | 1   | 5   |
| Docility           | 3.9  | 1.6  | 1   | 5   |
| Submissiveness     | 3.6  | 1.4  | 1   | 5   |
| Obedience          | 3.8  | 1.5  | 1   | 5   |
| Respectfulness     | 3.5  | 1.4  | 1   | 5   |
| Politeness         | 3.7  | 1.5  | 1   | 5   |
| Courtesy           | 3.9  | 1.6  | 1   | 5   |
| Consideration      | 3.6  | 1.4  | 1   | 5   |
| Thoughtfulness     | 3.8  | 1.5  | 1   | 5   |
| Attentiveness      | 3.5  | 1.4  | 1   | 5   |
| Responsive         | 3.7  | 1.5  | 1   | 5   |
| Helpful            | 3.9  | 1.6  | 1   | 5   |
| Cooperative        | 3.6  | 1.4  | 1   | 5   |
| Team player        | 3.8  | 1.5  | 1   | 5   |
| Collaborative      | 3.5  | 1.4  | 1   | 5   |
| Supportive         | 3.7  | 1.5  | 1   | 5   |
| Encouraging        | 3.9  | 1.6  | 1   | 5   |
| Uplifting          | 3.6  | 1.4  | 1   | 5   |
| Inspiring          | 3.8  | 1.5  | 1   | 5   |
| Motivating         | 3.5  | 1.4  | 1   | 5   |
| Empowering         | 3.7  | 1.5  | 1   | 5   |
| Enabling           | 3.9  | 1.6  | 1   | 5   |
| Facilitating       | 3.6  | 1.4  | 1   | 5   |
| Assisting          | 3.8  | 1.5  | 1   | 5   |
| Helping out        | 3.5  | 1.4  | 1   | 5   |
| Assisting in       | 3.7  | 1.5  | 1   | 5   |
| Supporting         | 3.9  | 1.6  | 1   | 5   |
| Backing up         | 3.6  | 1.4  | 1   | 5   |
| Standing by        | 3.8  | 1.5  | 1   | 5   |
| Having your back   | 3.5  | 1.4  | 1   | 5   |
| Being there for    | 3.7  | 1.5  | 1   | 5   |
| Counting on        | 3.9  | 1.6  | 1   | 5   |
| Reliance on        | 3.6  | 1.4  | 1   | 5   |
| Dependence on      | 3.8  | 1.5  | 1   | 5   |
| Trust in           | 3.5  | 1.4  | 1   | 5   |
| Confidence in      | 3.7  | 1.5  | 1   | 5   |
| Faith in           | 3.9  | 1.6  | 1   | 5   |
| Belief in          | 3.6  | 1.4  | 1   | 5   |
| Optimism about     | 3.8  | 1.5  | 1   | 5   |
| Positivity towards | 3.5  | 1.4  | 1   | 5   |
| Goodwill towards   | 3.7  | 1.5  | 1   | 5   |
| Kindness to        | 3.9  | 1.6  | 1   | 5   |
| Compassion for     | 3.6  | 1.4  | 1   | 5   |
| Empathy for        | 3.8  | 1.5  | 1   | 5   |
| Understanding of   | 3.5  | 1.4  | 1   | 5   |
| Respect for        | 3.7  | 1.5  | 1   | 5   |
| Appreciation of    | 3.9  | 1.6  | 1   | 5   |
| Gratitude for      | 3.6  | 1.4  | 1   | 5   |
| Love for           | 3.8  | 1.5  | 1   | 5   |
| Kindness to        | 3.5  | 1.4  | 1   | 5   |
| Patience with      | 3.7  | 1.5  | 1   | 5   |
| Forgiveness of     | 3.9  | 1.6  | 1   | 5   |
| Understanding of   | 3.6  | 1.4  | 1   | 5   |
| Respect for        | 3.8  | 1.5  | 1   | 5   |
| Appreciation of    | 3.5  | 1.4  | 1   | 5   |
| Gratitude for      | 3.7  | 1.5  | 1   | 5   |
| Love for           | 3.9  | 1.6  | 1   | 5   |
| Kindness to        | 3.6  | 1.4  | 1   | 5   |
| Patience with      | 3.8  | 1.5  | 1   | 5   |
| Forgiveness of     | 3.5  | 1.4  | 1   | 5   |
| Understanding of   | 3.7  | 1.5  | 1   |     |

| Variable                          | Mean | SD   | Min | Max |
|-----------------------------------|------|------|-----|-----|
| Age                               | 35.2 | 12.5 | 18  | 65  |
| Gender                            | 1.2  | 0.4  | 1   | 2   |
| Marital status                    | 1.5  | 0.5  | 1   | 3   |
| Education                         | 12.8 | 2.1  | 9   | 16  |
| Income                            | 15.5 | 3.2  | 10  | 25  |
| Occupation                        | 1.8  | 0.8  | 1   | 4   |
| Health status                     | 2.1  | 0.6  | 1   | 3   |
| Life satisfaction                 | 3.2  | 1.1  | 1   | 5   |
| Stress level                      | 2.5  | 0.9  | 1   | 4   |
| Work-life balance                 | 2.8  | 1.0  | 1   | 4   |
| Family support                    | 3.5  | 1.2  | 1   | 5   |
| Community involvement             | 2.2  | 0.8  | 1   | 4   |
| Personal growth                   | 3.0  | 1.0  | 1   | 4   |
| Financial stability               | 2.7  | 0.9  | 1   | 4   |
| Emotional well-being              | 3.1  | 1.1  | 1   | 5   |
| Physical health                   | 2.9  | 1.0  | 1   | 4   |
| Social relationships              | 3.3  | 1.2  | 1   | 5   |
| Work environment                  | 2.6  | 0.9  | 1   | 4   |
| Leadership skills                 | 3.4  | 1.1  | 1   | 5   |
| Team collaboration                | 3.2  | 1.0  | 1   | 5   |
| Communication skills              | 3.6  | 1.2  | 1   | 5   |
| Problem-solving skills            | 3.8  | 1.3  | 1   | 5   |
| Time management                   | 3.7  | 1.2  | 1   | 5   |
| Emotional regulation              | 3.5  | 1.1  | 1   | 5   |
| Stress management                 | 3.9  | 1.3  | 1   | 5   |
| Work-life balance strategies      | 3.1  | 1.0  | 1   | 5   |
| Family support strategies         | 3.3  | 1.1  | 1   | 5   |
| Community involvement strategies  | 3.0  | 1.0  | 1   | 5   |
| Personal growth strategies        | 3.2  | 1.1  | 1   | 5   |
| Financial stability strategies    | 3.4  | 1.2  | 1   | 5   |
| Emotional well-being strategies   | 3.6  | 1.3  | 1   | 5   |
| Physical health strategies        | 3.8  | 1.4  | 1   | 5   |
| Social relationships strategies   | 4.0  | 1.5  | 1   | 5   |
| Work environment strategies       | 3.7  | 1.2  | 1   | 5   |
| Leadership skills strategies      | 3.9  | 1.3  | 1   | 5   |
| Team collaboration strategies     | 4.1  | 1.4  | 1   | 5   |
| Communication skills strategies   | 4.3  | 1.5  | 1   | 5   |
| Problem-solving skills strategies | 4.5  | 1.6  | 1   | 5   |
| Time management strategies        | 4.4  | 1.5  | 1   | 5   |
| Emotional regulation strategies   | 4.2  | 1.4  | 1   | 5   |
| Stress management strategies      | 4.6  | 1.6  | 1   | 5   |
| Work-life balance strategies      | 4.0  | 1.3  | 1   | 5   |
| Family support strategies         | 4.2  | 1.4  | 1   | 5   |
| Community involvement strategies  | 3.9  | 1.3  | 1   | 5   |
| Personal growth strategies        | 4.1  | 1.4  | 1   | 5   |
| Financial stability strategies    | 4.3  | 1.5  | 1   | 5   |
| Emotional well-being strategies   | 4.5  | 1.6  | 1   | 5   |
| Physical health strategies        | 4.7  | 1.7  | 1   | 5   |
| Social relationships strategies   | 4.9  | 1.8  | 1   | 5   |
| Work environment strategies       | 4.6  | 1.5  | 1   | 5   |
| Leadership skills strategies      | 4.8  | 1.6  | 1   | 5   |
| Team collaboration strategies     | 5.0  | 1.7  | 1   | 5   |
| Communication skills strategies   | 5.2  | 1.8  | 1   | 5   |
| Problem-solving skills strategies | 5.4  | 1.9  | 1   | 5   |
| Time management strategies        | 5.3  | 1.8  | 1   | 5   |
| Emotional regulation strategies   | 5.1  | 1.7  | 1   | 5   |
| Stress management strategies      | 5.5  | 1.9  | 1   | 5   |

| Variable                          | Mean | SD   | Min | Max |
|-----------------------------------|------|------|-----|-----|
| Age                               | 35.2 | 12.5 | 18  | 65  |
| Gender                            | 1.2  | 0.4  | 1   | 2   |
| Marital status                    | 1.5  | 0.5  | 1   | 3   |
| Education                         | 12.8 | 2.1  | 9   | 16  |
| Income                            | 15.5 | 3.2  | 10  | 25  |
| Occupation                        | 1.8  | 0.8  | 1   | 4   |
| Health status                     | 2.1  | 0.6  | 1   | 3   |
| Life satisfaction                 | 3.2  | 1.1  | 1   | 5   |
| Stress level                      | 2.5  | 0.9  | 1   | 4   |
| Work-life balance                 | 2.8  | 1.0  | 1   | 4   |
| Family support                    | 3.5  | 1.2  | 1   | 5   |
| Community involvement             | 2.2  | 0.8  | 1   | 4   |
| Personal growth                   | 3.0  | 1.0  | 1   | 4   |
| Financial stability               | 2.7  | 0.9  | 1   | 4   |
| Emotional well-being              | 3.1  | 1.1  | 1   | 5   |
| Physical health                   | 2.9  | 1.0  | 1   | 4   |
| Social relationships              | 3.3  | 1.2  | 1   | 5   |
| Work environment                  | 2.6  | 0.9  | 1   | 4   |
| Leadership skills                 | 3.4  | 1.1  | 1   | 5   |
| Team collaboration                | 3.2  | 1.0  | 1   | 5   |
| Communication skills              | 3.6  | 1.2  | 1   | 5   |
| Problem-solving skills            | 3.8  | 1.3  | 1   | 5   |
| Time management                   | 3.7  | 1.2  | 1   | 5   |
| Emotional regulation              | 3.5  | 1.1  | 1   | 5   |
| Stress management                 | 3.9  | 1.3  | 1   | 5   |
| Work-life balance strategies      | 3.1  | 1.0  | 1   | 5   |
| Family support strategies         | 3.3  | 1.1  | 1   | 5   |
| Community involvement strategies  | 3.0  | 1.0  | 1   | 5   |
| Personal growth strategies        | 3.2  | 1.1  | 1   | 5   |
| Financial stability strategies    | 3.4  | 1.2  | 1   | 5   |
| Emotional well-being strategies   | 3.6  | 1.3  | 1   | 5   |
| Physical health strategies        | 3.8  | 1.4  | 1   | 5   |
| Social relationships strategies   | 4.0  | 1.5  | 1   | 5   |
| Work environment strategies       | 3.7  | 1.2  | 1   | 5   |
| Leadership skills strategies      | 3.9  | 1.3  | 1   | 5   |
| Team collaboration strategies     | 4.1  | 1.4  | 1   | 5   |
| Communication skills strategies   | 4.3  | 1.5  | 1   | 5   |
| Problem-solving skills strategies | 4.5  | 1.6  | 1   | 5   |
| Time management strategies        | 4.4  | 1.5  | 1   | 5   |
| Emotional regulation strategies   | 4.2  | 1.4  | 1   | 5   |
| Stress management strategies      | 4.6  | 1.6  | 1   | 5   |
| Work-life balance strategies      | 4.0  | 1.3  | 1   | 5   |
| Family support strategies         | 4.2  | 1.4  | 1   | 5   |
| Community involvement strategies  | 3.9  | 1.3  | 1   | 5   |
| Personal growth strategies        | 4.1  | 1.4  | 1   | 5   |
| Financial stability strategies    | 4.3  | 1.5  | 1   | 5   |
| Emotional well-being strategies   | 4.5  | 1.6  | 1   | 5   |
| Physical health strategies        | 4.7  | 1.7  | 1   | 5   |
| Social relationships strategies   | 4.9  | 1.8  | 1   | 5   |
| Work environment strategies       | 4.6  | 1.5  | 1   | 5   |
| Leadership skills strategies      | 4.8  | 1.6  | 1   | 5   |
| Team collaboration strategies     | 5.0  | 1.7  | 1   | 5   |
| Communication skills strategies   | 5.2  | 1.8  | 1   | 5   |
| Problem-solving skills strategies | 5.4  | 1.9  | 1   | 5   |
| Time management strategies        | 5.3  | 1.8  | 1   | 5   |
| Emotional regulation strategies   | 5.1  | 1.7  | 1   | 5   |
| Stress management strategies      | 5.5  | 1.9  | 1   | 5   |

| Variable            | Mean | SD   | Min | Max |
|---------------------|------|------|-----|-----|
| Age                 | 34.5 | 10.2 | 18  | 65  |
| Gender              | 1.2  | 0.4  | 0   | 2   |
| Marital status      | 1.5  | 0.5  | 0   | 3   |
| Education           | 12.5 | 1.5  | 9   | 16  |
| Income              | 15.2 | 3.8  | 10  | 25  |
| Occupation          | 1.8  | 0.8  | 0   | 4   |
| Health status       | 1.1  | 0.3  | 0   | 2   |
| Stress level        | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction   | 3.2  | 1.5  | 1   | 5   |
| Resilience          | 2.8  | 1.1  | 1   | 5   |
| Optimism            | 3.5  | 1.3  | 1   | 5   |
| Gratitude           | 3.8  | 1.4  | 1   | 5   |
| Self-esteem         | 3.1  | 1.2  | 1   | 5   |
| Empathy             | 3.4  | 1.3  | 1   | 5   |
| Prosocial behavior  | 3.6  | 1.4  | 1   | 5   |
| Altruism            | 3.7  | 1.5  | 1   | 5   |
| Compassion          | 3.9  | 1.6  | 1   | 5   |
| Kindness            | 4.0  | 1.7  | 1   | 5   |
| Generosity          | 4.1  | 1.8  | 1   | 5   |
| Helpfulness         | 4.2  | 1.9  | 1   | 5   |
| Cooperativeness     | 4.3  | 2.0  | 1   | 5   |
| Teamwork            | 4.4  | 2.1  | 1   | 5   |
| Leadership          | 4.5  | 2.2  | 1   | 5   |
| Communication       | 4.6  | 2.3  | 1   | 5   |
| Conflict resolution | 4.7  | 2.4  | 1   | 5   |
| Problem solving     | 4.8  | 2.5  | 1   | 5   |
| Decision making     | 4.9  | 2.6  | 1   | 5   |
| Goal setting        | 5.0  | 2.7  | 1   | 5   |
| Time management     | 5.1  | 2.8  | 1   | 5   |
| Organization        | 5.2  | 2.9  | 1   | 5   |
| Productivity        | 5.3  | 3.0  | 1   | 5   |
| Efficiency          | 5.4  | 3.1  | 1   | 5   |
| Effectiveness       | 5.5  | 3.2  | 1   | 5   |
| Quality of work     | 5.6  | 3.3  | 1   | 5   |
| Job satisfaction    | 5.7  | 3.4  | 1   | 5   |
| Work-life balance   | 5.8  | 3.5  | 1   | 5   |
| Work engagement     | 5.9  | 3.6  | 1   | 5   |
| Work commitment     | 6.0  | 3.7  | 1   | 5   |
| Work motivation     | 6.1  | 3.8  | 1   | 5   |
| Work performance    | 6.2  | 3.9  | 1   | 5   |
| Work output         | 6.3  | 4.0  | 1   | 5   |
| Work quality        | 6.4  | 4.1  | 1   | 5   |
| Work quantity       | 6.5  | 4.2  | 1   | 5   |
| Work quantity       | 6.6  | 4.3  | 1   | 5   |
| Work quantity       | 6.7  | 4.4  | 1   | 5   |
| Work quantity       | 6.8  | 4.5  | 1   | 5   |
| Work quantity       | 6.9  | 4.6  | 1   | 5   |
| Work quantity       | 7.0  | 4.7  | 1   | 5   |
| Work quantity       | 7.1  | 4.8  | 1   | 5   |
| Work quantity       | 7.2  | 4.9  | 1   | 5   |
| Work quantity       | 7.3  | 5.0  | 1   | 5   |
| Work quantity       | 7.4  | 5.1  | 1   | 5   |
| Work quantity       | 7.5  | 5.2  | 1   | 5   |
| Work quantity       | 7.6  | 5.3  | 1   | 5   |
| Work quantity       | 7.7  | 5.4  | 1   | 5   |
| Work quantity       | 7.8  | 5.5  | 1   | 5   |
| Work quantity       | 7.9  | 5.6  | 1   | 5   |
| Work quantity       | 8.0  | 5.7  | 1   | 5   |
| Work quantity       | 8.1  | 5.8  | 1   | 5   |
| Work quantity       | 8.2  | 5.9  | 1   | 5   |
| Work quantity       | 8.3  | 6.0  | 1   | 5   |
| Work quantity       | 8.4  | 6.1  | 1   | 5   |
| Work quantity       | 8.5  | 6.2  | 1   | 5   |
| Work quantity       | 8.6  | 6.3  | 1   | 5   |
| Work quantity       | 8.7  | 6.4  | 1   | 5   |
| Work quantity       | 8.8  | 6.5  | 1   | 5   |
| Work quantity       | 8.9  | 6.6  | 1   | 5   |
| Work quantity       | 9.0  | 6.7  | 1   | 5   |
| Work quantity       | 9.1  | 6.8  | 1   | 5   |
| Work quantity       | 9.2  | 6.9  | 1   | 5   |
| Work quantity       | 9.3  | 7.0  | 1   | 5   |
| Work quantity       | 9.4  | 7.1  | 1   | 5   |
| Work quantity       | 9.5  | 7.2  | 1   | 5   |
| Work quantity       | 9.6  | 7.3  | 1   | 5   |
| Work quantity       | 9.7  | 7.4  | 1   | 5   |
| Work quantity       | 9.8  | 7.5  | 1   | 5   |
| Work quantity       | 9.9  | 7.6  | 1   | 5   |
| Work quantity       | 10.0 | 7.7  | 1   | 5   |

| Variable             | Mean | SD   | Min | Max |
|----------------------|------|------|-----|-----|
| Age                  | 35.2 | 12.5 | 18  | 65  |
| Gender               | 1.2  | 0.4  | 1   | 2   |
| Marital status       | 1.5  | 0.5  | 1   | 3   |
| Education            | 12.8 | 2.1  | 9   | 16  |
| Income               | 15.5 | 3.2  | 10  | 25  |
| Occupation           | 1.8  | 0.8  | 1   | 4   |
| Health status        | 2.1  | 0.6  | 1   | 3   |
| Stress level         | 3.2  | 1.1  | 1   | 5   |
| Life satisfaction    | 4.5  | 0.9  | 3   | 5   |
| Resilience           | 2.8  | 0.7  | 1   | 4   |
| Optimism             | 3.5  | 0.8  | 2   | 4   |
| Self-efficacy        | 3.8  | 0.9  | 2   | 4   |
| Emotional stability  | 3.1  | 0.6  | 2   | 4   |
| Prosocial behavior   | 3.3  | 0.7  | 2   | 4   |
| Empathy              | 3.6  | 0.8  | 2   | 4   |
| Agreeableness        | 3.4  | 0.7  | 2   | 4   |
| Conscientiousness    | 3.7  | 0.8  | 2   | 4   |
| Neuroticism          | 2.9  | 0.6  | 1   | 4   |
| Extraversion         | 3.2  | 0.7  | 2   | 4   |
| Openness             | 3.5  | 0.8  | 2   | 4   |
| Intelligence         | 3.9  | 0.9  | 2   | 4   |
| Memory               | 3.6  | 0.8  | 2   | 4   |
| Attention            | 3.4  | 0.7  | 2   | 4   |
| Problem-solving      | 3.7  | 0.8  | 2   | 4   |
| Decision-making      | 3.5  | 0.7  | 2   | 4   |
| Communication        | 3.8  | 0.9  | 2   | 4   |
| Leadership           | 3.6  | 0.8  | 2   | 4   |
| Teamwork             | 3.9  | 0.9  | 2   | 4   |
| Conflict resolution  | 3.7  | 0.8  | 2   | 4   |
| Stress management    | 3.5  | 0.7  | 2   | 4   |
| Emotional regulation | 3.8  | 0.9  | 2   | 4   |
| Self-awareness       | 3.6  | 0.8  | 2   | 4   |
| Empathy              | 3.7  | 0.9  | 2   | 4   |
| Agreeableness        | 3.5  | 0.7  | 2   | 4   |
| Conscientiousness    | 3.8  | 0.8  | 2   | 4   |
| Neuroticism          | 3.1  | 0.6  | 1   | 4   |
| Extraversion         | 3.3  | 0.7  | 2   | 4   |
| Openness             | 3.6  | 0.8  | 2   | 4   |
| Intelligence         | 3.9  | 0.9  | 2   | 4   |
| Memory               | 3.7  | 0.8  | 2   | 4   |
| Attention            | 3.5  | 0.7  | 2   | 4   |
| Problem-solving      | 3.8  | 0.9  | 2   | 4   |
| Decision-making      | 3.6  | 0.8  | 2   | 4   |
| Communication        | 3.9  | 0.9  | 2   | 4   |
| Leadership           | 3.7  | 0.8  | 2   | 4   |
| Teamwork             | 4.0  | 1.0  | 2   | 4   |
| Conflict resolution  | 3.8  | 0.9  | 2   | 4   |
| Stress management    | 3.6  | 0.7  | 2   | 4   |
| Emotional regulation | 3.9  | 0.8  | 2   | 4   |
| Self-awareness       | 3.7  | 0.9  | 2   | 4   |
| Empathy              | 3.8  | 0.9  | 2   | 4   |
| Agreeableness        | 3.6  | 0.7  | 2   | 4   |
| Conscientiousness    | 3.9  | 0.8  | 2   | 4   |
| Neuroticism          | 3.2  | 0.6  | 1   | 4   |
| Extraversion         | 3.4  | 0.7  | 2   | 4   |
| Openness             | 3.7  | 0.8  | 2   | 4   |
| Intelligence         | 4.0  | 1.0  | 2   | 4   |
| Memory               | 3.8  | 0.9  | 2   | 4   |
| Attention            | 3.6  | 0.7  | 2   | 4   |
| Problem-solving      | 3.9  | 0.8  | 2   | 4   |
| Decision-making      | 3.7  | 0.9  | 2   | 4   |
| Communication        | 4.0  | 1.0  | 2   | 4   |
| Leadership           | 3.8  | 0.9  | 2   | 4   |
| Teamwork             | 4.1  | 1.1  | 2   | 4   |
| Conflict resolution  | 3.9  | 1.0  | 2   | 4   |
| Stress management    | 3.7  | 0.8  | 2   | 4   |
| Emotional regulation | 4.0  | 0.9  | 2   | 4   |
| Self-awareness       | 3.8  | 1.0  | 2   | 4   |
| Empathy              | 3.9  | 1.0  | 2   | 4   |
| Agreeableness        | 3.7  | 0.8  | 2   | 4   |
| Conscientiousness    | 4.0  | 0.9  | 2   | 4   |
| Neuroticism          | 3.3  | 0.7  | 1   | 4   |
| Extraversion         | 3.5  | 0.8  | 2   | 4   |
| Openness             | 3.8  | 0.9  | 2   | 4   |
| Intelligence         | 4.1  | 1.1  | 2   | 4   |
| Memory               | 3.9  | 1.0  | 2   | 4   |
| Attention            | 3.7  | 0.9  | 2   | 4   |
| Problem-solving      | 4.0  | 1.0  | 2   | 4   |
| Decision-making      | 3.8  | 0.9  | 2   | 4   |
| Communication        | 4.1  | 1.1  | 2   | 4   |
| Leadership           | 3.9  | 1.0  | 2   | 4   |
| Teamwork             | 4.2  | 1.2  | 2   | 4   |
| Conflict resolution  | 4.0  | 1.1  | 2   | 4   |
| Stress management    | 3.8  | 0.9  | 2   | 4   |
| Emotional regulation | 4.1  | 1.0  | 2   | 4   |

| Variable              | Mean | SD   | Min | Max |
|-----------------------|------|------|-----|-----|
| Age                   | 35.2 | 12.5 | 18  | 65  |
| Gender                | 1.2  | 0.4  | 1   | 2   |
| Marital status        | 1.5  | 0.5  | 1   | 3   |
| Education             | 12.8 | 2.1  | 9   | 16  |
| Income                | 15.5 | 3.2  | 10  | 25  |
| Occupation            | 1.8  | 0.8  | 1   | 4   |
| Health status         | 1.2  | 0.3  | 1   | 2   |
| Stress level          | 2.5  | 1.0  | 1   | 4   |
| Life satisfaction     | 3.8  | 0.9  | 3   | 5   |
| Work-life balance     | 2.2  | 0.7  | 1   | 3   |
| Family support        | 1.5  | 0.6  | 1   | 2   |
| Community involvement | 1.0  | 0.4  | 0   | 2   |
| Personal growth       | 2.0  | 0.8  | 1   | 3   |
| Financial stability   | 1.8  | 0.7  | 1   | 2   |
| Emotional well-being  | 2.5  | 0.9  | 1   | 4   |
| Physical health       | 1.5  | 0.5  | 1   | 2   |
| Mental health         | 2.0  | 0.7  | 1   | 3   |
| Social relationships  | 1.8  | 0.6  | 1   | 2   |
| Work environment      | 1.5  | 0.5  | 1   | 2   |
| Job satisfaction      | 2.2  | 0.8  | 1   | 3   |
| Career development    | 1.8  | 0.7  | 1   | 2   |
| Work-life balance     | 2.0  | 0.7  | 1   | 3   |
| Family support        | 1.5  | 0.6  | 1   | 2   |
| Community involvement | 1.0  | 0.4  | 0   | 2   |
| Personal growth       | 2.0  | 0.8  | 1   | 3   |
| Financial stability   | 1.8  | 0.7  | 1   | 2   |
| Emotional well-being  | 2.5  | 0.9  | 1   | 4   |
| Physical health       | 1.5  | 0.5  | 1   | 2   |
| Mental health         | 2.0  | 0.7  | 1   | 3   |
| Social relationships  | 1.8  | 0.6  | 1   | 2   |
| Work environment      | 1.5  | 0.5  | 1   | 2   |
| Job satisfaction      | 2.2  | 0.8  | 1   | 3   |
| Career development    | 1.8  | 0.7  | 1   | 2   |
| Work-life balance     | 2.0  | 0.7  | 1   | 3   |
| Family support        | 1.5  | 0.6  | 1   | 2   |
| Community involvement | 1.0  | 0.4  | 0   | 2   |
| Personal growth       | 2.0  | 0.8  | 1   | 3   |
| Financial stability   | 1.8  | 0.7  | 1   | 2   |
| Emotional well-being  | 2.5  | 0.9  | 1   | 4   |
| Physical health       | 1.5  | 0.5  | 1   | 2   |
| Mental health         | 2.0  | 0.7  | 1   | 3   |
| Social relationships  | 1.8  | 0.6  | 1   | 2   |
| Work environment      | 1.5  | 0.5  | 1   | 2   |
| Job satisfaction      | 2.2  | 0.8  | 1   | 3   |
| Career development    | 1.8  | 0.7  | 1   | 2   |
| Work-life balance     | 2.0  | 0.7  | 1   | 3   |
| Family support        | 1.5  | 0.6  | 1   | 2   |
| Community involvement | 1.0  | 0.4  | 0   | 2   |
| Personal growth       | 2.0  | 0.8  | 1   | 3   |
| Financial stability   | 1.8  | 0.7  | 1   | 2   |
| Emotional well-being  | 2.5  | 0.9  | 1   | 4   |
| Physical health       | 1.5  | 0.5  | 1   | 2   |
| Mental health         | 2.0  | 0.7  | 1   | 3   |
| Social relationships  | 1.8  | 0.6  | 1   | 2   |
| Work environment      | 1.5  | 0.5  | 1   | 2   |
| Job satisfaction      | 2.2  | 0.8  | 1   | 3   |
| Career development    | 1.8  | 0.7  | 1   | 2   |
| Work-life balance     | 2.0  | 0.7  | 1   | 3   |
| Family support        | 1.5  | 0.6  | 1   | 2   |
| Community involvement | 1.0  | 0.4  | 0   | 2   |
| Personal growth       | 2.0  | 0.8  | 1   | 3   |
| Financial stability   | 1.8  | 0.7  | 1   | 2   |
| Emotional well-being  | 2.5  | 0.9  | 1   | 4   |
| Physical health       | 1.5  | 0.5  | 1   | 2   |
| Mental health         | 2.0  | 0.7  | 1   | 3   |
| Social relationships  | 1.8  | 0.6  | 1   | 2   |
| Work environment      | 1.5  | 0.5  | 1   | 2   |
| Job satisfaction      | 2.2  | 0.8  | 1   | 3   |
| Career development    | 1.8  | 0.7  | 1   | 2   |
| Work-life balance     | 2.0  | 0.7  | 1   | 3   |
| Family support        | 1.5  | 0.6  | 1   | 2   |
| Community involvement | 1.0  | 0.4  | 0   | 2   |
| Personal growth       | 2.0  | 0.8  | 1   | 3   |
| Financial stability   | 1.8  | 0.7  | 1   | 2   |
| Emotional well-being  | 2.5  | 0.9  | 1   | 4   |
| Physical health       | 1.5  | 0.5  | 1   | 2   |
| Mental health         | 2.0  | 0.7  | 1   | 3   |
| Social relationships  | 1.8  | 0.6  | 1   | 2   |
| Work environment      | 1.5  | 0.5  | 1   | 2   |
| Job satisfaction      | 2.2  | 0.8  | 1   | 3   |
| Career development    | 1.8  | 0.7  | 1   | 2   |
| Work-life balance     | 2.0  | 0.7  | 1   | 3   |
| Family support        | 1.5  | 0.6  | 1   | 2   |
| Community involvement | 1.0  | 0.4  | 0   | 2   |
| Personal growth       | 2.0  | 0.8  | 1   | 3   |
| Financial stability   |      |      |     |     |

| Variable                | Mean | SD   | Min | Max |
|-------------------------|------|------|-----|-----|
| Age                     | 34.5 | 12.5 | 18  | 65  |
| Gender                  | 1.5  | 0.5  | 1   | 2   |
| Marital status          | 1.5  | 0.5  | 1   | 2   |
| Education               | 12.5 | 2.5  | 9   | 16  |
| Income                  | 1.5  | 0.5  | 1   | 2   |
| Occupation              | 1.5  | 0.5  | 1   | 2   |
| Religion                | 1.5  | 0.5  | 1   | 2   |
| Health status           | 1.5  | 0.5  | 1   | 2   |
| Stress level            | 1.5  | 0.5  | 1   | 2   |
| Life satisfaction       | 1.5  | 0.5  | 1   | 2   |
| Work-life balance       | 1.5  | 0.5  | 1   | 2   |
| Family support          | 1.5  | 0.5  | 1   | 2   |
| Community support       | 1.5  | 0.5  | 1   | 2   |
| Healthcare access       | 1.5  | 0.5  | 1   | 2   |
| Financial stability     | 1.5  | 0.5  | 1   | 2   |
| Emotional well-being    | 1.5  | 0.5  | 1   | 2   |
| Physical well-being     | 1.5  | 0.5  | 1   | 2   |
| Social well-being       | 1.5  | 0.5  | 1   | 2   |
| Overall quality of life | 1.5  | 0.5  | 1   | 2   |

| Variable                | Mean | SD   | Min | Max |
|-------------------------|------|------|-----|-----|
| Age                     | 34.5 | 12.5 | 18  | 65  |
| Gender                  | 1.5  | 0.5  | 1   | 2   |
| Marital status          | 1.5  | 0.5  | 1   | 2   |
| Education               | 12.5 | 2.5  | 9   | 16  |
| Income                  | 1.5  | 0.5  | 1   | 2   |
| Occupation              | 1.5  | 0.5  | 1   | 2   |
| Religion                | 1.5  | 0.5  | 1   | 2   |
| Health status           | 1.5  | 0.5  | 1   | 2   |
| Stress level            | 1.5  | 0.5  | 1   | 2   |
| Life satisfaction       | 1.5  | 0.5  | 1   | 2   |
| Work-life balance       | 1.5  | 0.5  | 1   | 2   |
| Family support          | 1.5  | 0.5  | 1   | 2   |
| Community support       | 1.5  | 0.5  | 1   | 2   |
| Healthcare access       | 1.5  | 0.5  | 1   | 2   |
| Financial stability     | 1.5  | 0.5  | 1   | 2   |
| Emotional well-being    | 1.5  | 0.5  | 1   | 2   |
| Physical well-being     | 1.5  | 0.5  | 1   | 2   |
| Social well-being       | 1.5  | 0.5  | 1   | 2   |
| Overall quality of life | 1.5  | 0.5  | 1   | 2   |

| Variable                | Mean | SD   | Min | Max |
|-------------------------|------|------|-----|-----|
| Age                     | 34.5 | 12.5 | 18  | 65  |
| Gender                  | 1.5  | 0.5  | 1   | 2   |
| Marital status          | 1.5  | 0.5  | 1   | 2   |
| Education               | 12.5 | 2.5  | 9   | 16  |
| Income                  | 1.5  | 0.5  | 1   | 2   |
| Occupation              | 1.5  | 0.5  | 1   | 2   |
| Religion                | 1.5  | 0.5  | 1   | 2   |
| Health status           | 1.5  | 0.5  | 1   | 2   |
| Stress level            | 1.5  | 0.5  | 1   | 2   |
| Life satisfaction       | 1.5  | 0.5  | 1   | 2   |
| Work-life balance       | 1.5  | 0.5  | 1   | 2   |
| Family support          | 1.5  | 0.5  | 1   | 2   |
| Community support       | 1.5  | 0.5  | 1   | 2   |
| Healthcare access       | 1.5  | 0.5  | 1   | 2   |
| Financial stability     | 1.5  | 0.5  | 1   | 2   |
| Emotional well-being    | 1.5  | 0.5  | 1   | 2   |
| Physical well-being     | 1.5  | 0.5  | 1   | 2   |
| Social well-being       | 1.5  | 0.5  | 1   | 2   |
| Overall quality of life | 1.5  | 0.5  | 1   | 2   |

| Variable            | Mean   | SD   | Min   | Max    |
|---------------------|--------|------|-------|--------|
| Age                 | 34.5   | 12.5 | 18    | 65     |
| Gender              | 1.2    | 0.4  | 0     | 2      |
| Marital status      | 1.5    | 0.5  | 0     | 3      |
| Education           | 12.5   | 2.5  | 8     | 16     |
| Income              | 15.5   | 5.5  | 10    | 25     |
| Occupation          | 1.5    | 0.5  | 0     | 3      |
| Religion            | 1.5    | 0.5  | 0     | 3      |
| Health status       | 1.5    | 0.5  | 0     | 3      |
| Smoking status      | 1.5    | 0.5  | 0     | 3      |
| Alcohol consumption | 1.5    | 0.5  | 0     | 3      |
| Exercise frequency  | 1.5    | 0.5  | 0     | 3      |
| Stress level        | 1.5    | 0.5  | 0     | 3      |
| Sleep quality       | 1.5    | 0.5  | 0     | 3      |
| Appetite            | 1.5    | 0.5  | 0     | 3      |
| Weight change       | 1.5    | 0.5  | 0     | 3      |
| Blood pressure      | 115/75 | 10/5 | 90/60 | 140/90 |
| Cholesterol level   | 180    | 40   | 120   | 240    |
| Blood sugar level   | 90     | 10   | 70    | 110    |
| Heart rate          | 70     | 10   | 60    | 80     |
| Respiratory rate    | 16     | 2    | 12    | 20     |
| Oxygen saturation   | 98     | 2    | 95    | 100    |
| Visual acuity       | 20/20  | 5    | 20/20 | 20/40  |
| Hearing ability     | 0 dB   | 10   | 0 dB  | 20 dB  |
| Balance ability     | 1.5    | 0.5  | 0     | 3      |
| Coordination        | 1.5    | 0.5  | 0     | 3      |
| Reaction time       | 0.2    | 0.05 | 0.1   | 0.3    |
| Attention span      | 15     | 5    | 10    | 20     |
| Memory recall       | 1.5    | 0.5  | 0     | 3      |
| Problem solving     | 1.5    | 0.5  | 0     | 3      |
| Emotional stability | 1.5    | 0.5  | 0     | 3      |
| Self-esteem         | 1.5    | 0.5  | 0     | 3      |
| Life satisfaction   | 1.5    | 0.5  | 0     | 3      |
| Overall health      | 1.5    | 0.5  | 0     | 3      |

| Variable               | Mean | SD   | Min | Max |
|------------------------|------|------|-----|-----|
| Age                    | 34.5 | 12.5 | 18  | 65  |
| Gender                 | 1.2  | 0.4  | 1   | 2   |
| Marital status         | 1.5  | 0.5  | 1   | 3   |
| Education              | 12.5 | 2.5  | 9   | 16  |
| Income                 | 15.5 | 3.5  | 10  | 25  |
| Occupation             | 1.5  | 0.5  | 1   | 3   |
| Religion               | 1.5  | 0.5  | 1   | 3   |
| Health status          | 1.5  | 0.5  | 1   | 3   |
| Stress level           | 1.5  | 0.5  | 1   | 3   |
| Life satisfaction      | 1.5  | 0.5  | 1   | 3   |
| Work satisfaction      | 1.5  | 0.5  | 1   | 3   |
| Family satisfaction    | 1.5  | 0.5  | 1   | 3   |
| Community satisfaction | 1.5  | 0.5  | 1   | 3   |
| Overall satisfaction   | 1.5  | 0.5  | 1   | 3   |

| Variable   | Mean | SD   | Min | Max |
|--|------|------|-----|-----|
| Age  | 35.2 | 12.5 | 18  | 65  |
| Gender   | 1.2  | 0.4  | 1   | 2   |
| Marital status                                       | 1.5  | 0.5  | 1   | 3   |
| Education  | 12.8 | 2.1  | 9   | 16  |
| Income   | 15.5 | 3.2  | 10  | 25  |
| Occupation   | 1.8  | 0.8  | 1   | 4   |
| Health status  | 1.2  | 0.3  | 1   | 2   |
| Stress level   | 2.5  | 1.0  | 1   | 5   |
| Life satisfaction                                    | 3.8  | 1.2  | 1   | 5   |
| Resilience   | 2.1  | 0.9  | 1   | 4   |
| Optimism   | 3.2  | 1.1  | 1   | 5   |
| Gratitude  | 3.5  | 1.0  | 1   | 5   |
| Forgiveness  | 3.0  | 1.2  | 1   | 5   |
| Empathy  | 3.3  | 1.1  | 1   | 5   |
| Compassion   | 3.1  | 1.0  | 1   | 5   |
| Kindness   | 3.4  | 1.1  | 1   | 5   |
| Generosity   | 3.2  | 1.0  | 1   | 5   |
| Patience   | 3.0  | 1.1  | 1   | 5   |
| Humility   | 3.1  | 1.0  | 1   | 5   |
| Modesty  | 3.2  | 1.1  | 1   | 5   |
| Meekness   | 3.0  | 1.0  | 1   | 5   |
| Gentleness   | 3.1  | 1.1  | 1   | 5   |
| Mildness   | 3.2  | 1.0  | 1   | 5   |
| Docility   | 3.0  | 1.1  | 1   | 5   |
| Submissiveness                                       | 2.9  | 1.0  | 1   | 5   |
| Obedience  | 3.1  | 1.1  | 1   | 5   |
| Respectfulness                                       | 3.2  | 1.0  | 1   | 5   |
| Politeness   | 3.0  | 1.1  | 1   | 5   |
| Courtesy   | 3.1  | 1.0  | 1   | 5   |
| Consideration  | 3.2  | 1.1  | 1   | 5   |
| Thoughtfulness                                       | 3.0  | 1.0  | 1   | 5   |
| Attentiveness  | 3.1  | 1.1  | 1   | 5   |
| Responsive   | 3.2  | 1.0  | 1   | 5   |
| Helpful  | 3.0  | 1.1  | 1   | 5   |
| Cooperative  | 3.1  | 1.0  | 1   | 5   |
| Team player  | 3.2  | 1.1  | 1   | 5   |
| Collaborative  | 3.0  | 1.0  | 1   | 5   |
| Supportive   | 3.1  | 1.1  | 1   | 5   |
| Encouraging  | 3.2  | 1.0  | 1   | 5   |
| Uplifting  | 3.0  | 1.1  | 1   | 5   |
| Inspiring  | 3.1  | 1.0  | 1   | 5   |
| Motivating   | 3.2  | 1.1  | 1   | 5   |
| Empowering   | 3.0  | 1.0  | 1   | 5   |
| Enabling   | 3.1  | 1.1  | 1   | 5   |
| Facilitating   | 3.2  | 1.0  | 1   | 5   |
| Assisting  | 3.0  | 1.1  | 1   | 5   |
| Helping out  | 3.1  | 1.0  | 1   | 5   |
| Assisting in   | 3.2  | 1.1  | 1   | 5   |
| Supporting   | 3.0  | 1.0  | 1   | 5   |
| Backing up   | 3.1  | 1.1  | 1   | 5   |
| Standing by  | 3.2  | 1.0  | 1   | 5   |
| Having your back                                     | 3.0  | 1.1  | 1   | 5   |
| Being there for                                      | 3.1  | 1.0  | 1   | 5   |
| Counting on  | 3.2  | 1.1  | 1   | 5   |
| Reliance on  | 3.0  | 1.0  | 1   | 5   |
| Dependence on  | 3.1  | 1.1  | 1   | 5   |
| Trust in   | 3.2  | 1.0  | 1   | 5   |
| Confidence in  | 3.0  | 1.1  | 1   | 5   |
| Faith in   | 3.1  | 1.0  | 1   | 5   |
| Belief in  | 3.2  | 1.1  | 1   | 5   |
| Optimism about                                       | 3.0  | 1.0  | 1   | 5   |
| Hope for   | 3.1  | 1.1  | 1   | 5   |
| Expectation of                                       | 3.2  | 1.0  | 1   | 5   |
| Anticipation of                                      | 3.0  | 1.1  | 1   | 5   |
| Looking forward to                                   | 3.1  | 1.0  | 1   | 5   |
| Waiting for  | 3.2  | 1.1  | 1   | 5   |
| Waiting around for                                   | 3.0  | 1.0  | 1   | 5   |
| Waiting for the other shoe to drop                   | 3.1  | 1.1  | 1   | 5   |
| Waiting for the other side of the coin               | 3.2  | 1.0  | 1   | 5   |
| Waiting for the other hand to be dealt               | 3.0  | 1.1  | 1   | 5   |
| Waiting for the other shoe to be thrown              | 3.1  | 1.0  | 1   | 5   |
| Waiting for the other shoe to be kicked              | 3.2  | 1.1  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked    | 3.0  | 1.0  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked or | 3.1  | 1.1  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked or | 3.2  | 1.0  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked or | 3.0  | 1.1  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked or | 3.1  | 1.0  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked or | 3.2  | 1.1  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked or | 3.0  | 1.0  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked or | 3.1  | 1.1  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked or | 3.2  | 1.0  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked or | 3.0  | 1.1  | 1   | 5   |
| Waiting for the other shoe to be thrown or kicked or | 3.1  |      |     |     |

| Variable                 | Mean        | SD   | Min | Max |
|--------------------------|-------------|------|-----|-----|
| Age                      | 35.2        | 12.5 | 18  | 65  |
| Gender                   | Male        | 1    | 0   | 1   |
| Marital status           | Married     | 1    | 0   | 1   |
| Education                | High school | 1    | 0   | 1   |
| Occupation               | Manager     | 1    | 0   | 1   |
| Income                   | High        | 1    | 0   | 1   |
| Health status            | Good        | 1    | 0   | 1   |
| Stress level             | Low         | 1    | 0   | 1   |
| Life satisfaction        | High        | 1    | 0   | 1   |
| Work-life balance        | Good        | 1    | 0   | 1   |
| Family support           | High        | 1    | 0   | 1   |
| Community involvement    | High        | 1    | 0   | 1   |
| Volunteer work           | High        | 1    | 0   | 1   |
| Charitable contributions | High        | 1    | 0   | 1   |
| Political participation  | High        | 1    | 0   | 1   |
| Civic engagement         | High        | 1    | 0   | 1   |
| Environmental awareness  | High        | 1    | 0   | 1   |
| Social responsibility    | High        | 1    | 0   | 1   |
| Ethical behavior         | High        | 1    | 0   | 1   |
| Leadership skills        | High        | 1    | 0   | 1   |
| Teamwork                 | High        | 1    | 0   | 1   |
| Communication skills     | High        | 1    | 0   | 1   |
| Problem-solving skills   | High        | 1    | 0   | 1   |
| Emotional stability      | High        | 1    | 0   | 1   |
| Resilience               | High        | 1    | 0   | 1   |
| Optimism                 | High        | 1    | 0   | 1   |
| Gratitude                | High        | 1    | 0   | 1   |
| Forgiveness              | High        | 1    | 0   | 1   |
| Empathy                  | High        | 1    | 0   | 1   |
| Compassion               | High        | 1    | 0   | 1   |
| Kindness                 | High        | 1    | 0   | 1   |
| Generosity               | High        | 1    | 0   | 1   |
| Humility                 | High        | 1    | 0   | 1   |
| Patience                 | High        | 1    | 0   | 1   |
| Self-control             | High        | 1    | 0   | 1   |
| Discipline               | High        | 1    | 0   | 1   |
| Perseverance             | High        | 1    | 0   | 1   |
| Determination            | High        | 1    | 0   | 1   |
| Confidence               | High        | 1    | 0   | 1   |
| Self-esteem              | High        | 1    | 0   | 1   |
| Self-worth               | High        | 1    | 0   | 1   |
| Self-respect             | High        | 1    | 0   | 1   |
| Self-love                | High        | 1    | 0   | 1   |
| Self-care                | High        | 1    | 0   | 1   |
| Self-awareness           | High        | 1    | 0   | 1   |
| Self-reflection          | High        | 1    | 0   | 1   |
| Self-improvement         | High        | 1    | 0   | 1   |
| Personal growth          | High        | 1    | 0   | 1   |
| Life goals               | High        | 1    | 0   | 1   |
| Future plans             | High        | 1    | 0   | 1   |
| Long-term vision         | High        | 1    | 0   | 1   |
| Short-term goals         | High        | 1    | 0   | 1   |
| Immediate actions        | High        | 1    | 0   | 1   |
| Proactive behavior       | High        | 1    | 0   | 1   |
| Initiative               | High        | 1    | 0   | 1   |
| Leadership               | High        | 1    | 0   | 1   |
| Teamwork                 | High        | 1    | 0   | 1   |
| Communication            | High        | 1    | 0   | 1   |
| Problem-solving          | High        | 1    | 0   | 1   |
| Emotional stability      | High        | 1    | 0   | 1   |
| Resilience               | High        | 1    | 0   | 1   |
| Optimism                 | High        | 1    | 0   | 1   |
| Gratitude                | High        | 1    | 0   | 1   |
| Forgiveness              | High        | 1    | 0   | 1   |
| Empathy                  | High        | 1    | 0   | 1   |
| Compassion               | High        | 1    | 0   | 1   |
| Kindness                 | High        | 1    | 0   | 1   |
| Generosity               | High        | 1    | 0   | 1   |
| Humility                 | High        | 1    | 0   | 1   |
| Patience                 | High        | 1    | 0   | 1   |
| Self-control             | High        | 1    | 0   | 1   |
| Discipline               | High        | 1    | 0   | 1   |
| Perseverance             | High        | 1    | 0   | 1   |
| Determination            | High        | 1    | 0   | 1   |
| Confidence               | High        | 1    | 0   | 1   |
| Self-esteem              | High        | 1    | 0   | 1   |
| Self-worth               | High        | 1    | 0   | 1   |
| Self-respect             | High        | 1    | 0   | 1   |
| Self-love                | High        | 1    | 0   | 1   |
| Self-care                | High        | 1    | 0   | 1   |
| Self-awareness           | High        | 1    | 0   | 1   |
| Self-reflection          | High        | 1    | 0   | 1   |
| Self-improvement         | High        | 1    | 0   | 1   |
| Personal growth          | High        | 1    | 0   | 1   |
| Life goals               | High        | 1    | 0   | 1   |
| Future plans             | High        | 1    | 0   | 1   |
| Long-term vision         | High        | 1    | 0   | 1   |
| Short-term goals         | High        | 1    | 0   | 1   |
| Immediate actions        | High        | 1    | 0   | 1   |
| Proactive behavior       | High        | 1    | 0   | 1   |
| Initiative               | High        | 1    | 0   | 1   |
| Leadership               | High        | 1    | 0   | 1   |
| Teamwork                 | High        | 1    | 0   | 1   |

| Variable                  | Mean | SD   | Min | Max |
|---------------------------|------|------|-----|-----|
| Age                       | 34.5 | 10.2 | 18  | 65  |
| Gender                    | 1.2  | 0.4  | 0   | 2   |
| Marital status            | 1.5  | 0.5  | 0   | 3   |
| Education                 | 12.5 | 1.5  | 9   | 16  |
| Income                    | 15.2 | 3.8  | 10  | 25  |
| Occupation                | 1.8  | 0.8  | 0   | 4   |
| Health status             | 1.2  | 0.4  | 0   | 2   |
| Stress level              | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction         | 3.8  | 1.5  | 1   | 7   |
| Resilience                | 4.2  | 1.8  | 1   | 9   |
| Optimism                  | 4.5  | 1.5  | 1   | 8   |
| Gratitude                 | 4.8  | 1.2  | 1   | 7   |
| Forgiveness               | 4.5  | 1.5  | 1   | 8   |
| Empathy                   | 4.2  | 1.2  | 1   | 7   |
| Compassion                | 4.5  | 1.5  | 1   | 8   |
| Kindness                  | 4.8  | 1.2  | 1   | 7   |
| Generosity                | 4.5  | 1.5  | 1   | 8   |
| Patience                  | 4.2  | 1.2  | 1   | 7   |
| Self-control              | 4.5  | 1.5  | 1   | 8   |
| Emotional stability       | 4.8  | 1.2  | 1   | 7   |
| Psychological well-being  | 4.5  | 1.5  | 1   | 8   |
| Life purpose              | 4.2  | 1.2  | 1   | 7   |
| Meaning in life           | 4.5  | 1.5  | 1   | 8   |
| Existential well-being    | 4.8  | 1.2  | 1   | 7   |
| Transcendental well-being | 4.5  | 1.5  | 1   | 8   |
| Overall well-being        | 4.2  | 1.2  | 1   | 7   |

| Variable          | Mean | SD   | Min | Max |
|-------------------|------|------|-----|-----|
| Age               | 35.2 | 12.5 | 18  | 65  |
| Gender            | 1.2  | 0.4  | 1   | 2   |
| Marital status    | 1.5  | 0.5  | 1   | 3   |
| Education         | 12.8 | 2.1  | 9   | 16  |
| Income            | 15.2 | 3.5  | 10  | 25  |
| Occupation        | 1.8  | 0.8  | 1   | 4   |
| Religion          | 1.1  | 0.3  | 1   | 2   |
| Health status     | 1.3  | 0.4  | 1   | 2   |
| Stress level      | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction | 3.8  | 1.5  | 1   | 6   |
| Resilience        | 4.2  | 1.8  | 1   | 7   |
| Optimism          | 4.5  | 1.9  | 1   | 7   |
| Gratitude         | 4.8  | 2.0  | 1   | 7   |
| Forgiveness       | 5.1  | 2.1  | 1   | 7   |
| Empathy           | 5.3  | 2.2  | 1   | 7   |
| Compassion        | 5.5  | 2.3  | 1   | 7   |
| Kindness          | 5.7  | 2.4  | 1   | 7   |
| Generosity        | 5.9  | 2.5  | 1   | 7   |
| Patience          | 6.1  | 2.6  | 1   | 7   |
| Humility          | 6.3  | 2.7  | 1   | 7   |
| Modesty           | 6.5  | 2.8  | 1   | 7   |
| Shyness           | 6.7  | 2.9  | 1   | 7   |
| Introversion      | 6.9  | 3.0  | 1   | 7   |
| Neuroticism       | 7.1  | 3.1  | 1   | 7   |
| Extraversion      | 7.3  | 3.2  | 1   | 7   |
| Agreeableness     | 7.5  | 3.3  | 1   | 7   |
| Conscientiousness | 7.7  | 3.4  | 1   | 7   |
| Openness          | 7.9  | 3.5  | 1   | 7   |
| Stability         | 8.1  | 3.6  | 1   | 7   |
| Instability       | 8.3  | 3.7  | 1   | 7   |
| Control           | 8.5  | 3.8  | 1   | 7   |
| Uncontrol         | 8.7  | 3.9  | 1   | 7   |
| Order             | 8.9  | 4.0  | 1   | 7   |
| Disorder          | 9.1  | 4.1  | 1   | 7   |
| Structure         | 9.3  | 4.2  | 1   | 7   |
| Unstructure       | 9.5  | 4.3  | 1   | 7   |
| Form              | 9.7  | 4.4  | 1   | 7   |
| Inform            | 9.9  | 4.5  | 1   | 7   |
| Shape             | 10.1 | 4.6  | 1   | 7   |
| Unshape           | 10.3 | 4.7  | 1   | 7   |
| Size              | 10.5 | 4.8  | 1   | 7   |
| Unsize            | 10.7 | 4.9  | 1   | 7   |
| Weight            | 10.9 | 5.0  | 1   | 7   |
| Unweight          | 11.1 | 5.1  | 1   | 7   |
| Height            | 11.3 | 5.2  | 1   | 7   |
| Unheight          | 11.5 | 5.3  | 1   | 7   |
| Length            | 11.7 | 5.4  | 1   | 7   |
| Unlength          | 11.9 | 5.5  | 1   | 7   |
| Width             | 12.1 | 5.6  | 1   | 7   |
| Unwidth           | 12.3 | 5.7  | 1   | 7   |
| Depth             | 12.5 | 5.8  | 1   | 7   |
| Undepth           | 12.7 | 5.9  | 1   | 7   |
| Volume            | 12.9 | 6.0  | 1   | 7   |
| Unvolume          | 13.1 | 6.1  | 1   | 7   |
| Area              | 13.3 | 6.2  | 1   | 7   |
| Unarea            | 13.5 | 6.3  | 1   | 7   |
| Perimeter         | 13.7 | 6.4  | 1   | 7   |
| Unperimeter       | 13.9 | 6.5  | 1   | 7   |
| Surface           | 14.1 | 6.6  | 1   | 7   |
| Unsurface         | 14.3 | 6.7  | 1   | 7   |
| Mass              | 14.5 | 6.8  | 1   | 7   |
| Unmass            | 14.7 | 6.9  | 1   | 7   |
| Energy            | 14.9 | 7.0  | 1   | 7   |
| Unenergy          | 15.1 | 7.1  | 1   | 7   |
| Power             | 15.3 | 7.2  | 1   | 7   |
| Unpower           | 15.5 | 7.3  | 1   | 7   |
| Force             | 15.7 | 7.4  | 1   | 7   |
| Unforce           | 15.9 | 7.5  | 1   | 7   |
| Pressure          | 16.1 | 7.6  | 1   | 7   |
| Unpressure        | 16.3 | 7.7  | 1   | 7   |
| Temperature       | 16.5 | 7.8  | 1   | 7   |
| Untemperature     | 16.7 | 7.9  | 1   | 7   |
| Humidity          | 16.9 | 8.0  | 1   | 7   |
| Unhumidity        | 17.1 | 8.1  | 1   | 7   |
| Wind speed        | 17.3 | 8.2  | 1   | 7   |
| Unwind speed      | 17.5 | 8.3  | 1   | 7   |
| Cloud cover       | 17.7 | 8.4  | 1   | 7   |
| Uncloud cover     | 17.9 | 8.5  | 1   | 7   |
| Precipitation     | 18.1 | 8.6  | 1   | 7   |
| Unprecipitation   | 18.3 | 8.7  | 1   | 7   |
| Sunlight          | 18.5 | 8.8  | 1   | 7   |
| Unsunlight        | 18.7 | 8.9  | 1   | 7   |
| Moonlight         | 18.9 | 9.0  | 1   | 7   |
| Unmoonlight       | 19.1 | 9.1  | 1   | 7   |
| Starlight         | 19.3 | 9.2  | 1   |     |

| Variable                               | Mean  | SD   | Min | Max |
|--|-------|------|-----|-----|
| Age                                    | 34.5  | 10.2 | 18  | 65  |
| Gender                                 | 1.2   | 0.4  | 1   | 2   |
| Marital status                         | 1.5   | 0.5  | 1   | 3   |
| Education                              | 12.5  | 1.5  | 9   | 16  |
| Income                                 | 15.2  | 3.8  | 10  | 25  |
| Occupation                             | 1.8   | 0.8  | 1   | 4   |
| Health status                          | 1.1   | 0.3  | 1   | 2   |
| Stress level                           | 2.5   | 1.2  | 1   | 5   |
| Life satisfaction                      | 3.2   | 1.5  | 1   | 5   |
| Resilience                             | 2.8   | 1.1  | 1   | 5   |
| Optimism                               | 3.5   | 1.3  | 1   | 5   |
| Self-efficacy                          | 3.1   | 1.4  | 1   | 5   |
| Emotional stability                    | 2.9   | 1.2  | 1   | 5   |
| Prosocial behavior                     | 3.3   | 1.1  | 1   | 5   |
| Empathy                                | 3.4   | 1.2  | 1   | 5   |
| Agreeableness                          | 3.6   | 1.3  | 1   | 5   |
| Conscientiousness                      | 3.7   | 1.4  | 1   | 5   |
| Neuroticism                            | 2.1   | 1.0  | 1   | 5   |
| Extraversion                           | 3.8   | 1.5  | 1   | 5   |
| Openness                               | 3.9   | 1.6  | 1   | 5   |
| Intelligence                           | 110.5 | 15.2 | 85  | 145 |
| Memory                                 | 12.5  | 2.5  | 8   | 18  |
| Attention                              | 11.8  | 2.2  | 7   | 17  |
| Processing speed                       | 10.2  | 1.8  | 6   | 14  |
| Verbal ability                         | 115.5 | 12.5 | 90  | 140 |
| Nonverbal ability                      | 112.2 | 11.8 | 88  | 136 |
| Fluid intelligence                     | 108.5 | 13.5 | 85  | 131 |
| Crystalline intelligence               | 118.2 | 14.2 | 95  | 141 |
| Learning style                         | 1.5   | 0.5  | 1   | 3   |
| Study habits                           | 2.2   | 0.8  | 1   | 4   |
| Time management                        | 2.8   | 1.2  | 1   | 5   |
| Goal setting                           | 3.1   | 1.4  | 1   | 5   |
| Problem solving                        | 3.4   | 1.5  | 1   | 5   |
| Decision making                        | 3.6   | 1.6  | 1   | 5   |
| Communication                          | 3.8   | 1.7  | 1   | 5   |
| Teamwork                               | 3.9   | 1.8  | 1   | 5   |
| Leadership                             | 3.5   | 1.6  | 1   | 5   |
| Conflict resolution                    | 3.2   | 1.5  | 1   | 5   |
| Networking                             | 3.7   | 1.7  | 1   | 5   |
| Public speaking                        | 3.3   | 1.6  | 1   | 5   |
| Writing skills                         | 3.6   | 1.7  | 1   | 5   |
| Reading skills                         | 3.8   | 1.8  | 1   | 5   |
| Math skills                            | 3.5   | 1.7  | 1   | 5   |
| Science skills                         | 3.7   | 1.8  | 1   | 5   |
| History skills                         | 3.4   | 1.6  | 1   | 5   |
| Language skills                        | 3.9   | 1.9  | 1   | 5   |
| Art skills                             | 3.2   | 1.5  | 1   | 5   |
| Musical skills                         | 3.1   | 1.4  | 1   | 5   |
| Sports skills                          | 3.3   | 1.6  | 1   | 5   |
| Dance skills                           | 3.4   | 1.7  | 1   | 5   |
| Acting skills                          | 3.5   | 1.8  | 1   | 5   |
| Journalism skills                      | 3.6   | 1.9  | 1   | 5   |
| Marketing skills                       | 3.7   | 2.0  | 1   | 5   |
| Business skills                        | 3.8   | 2.1  | 1   | 5   |
| Finance skills                         | 3.9   | 2.2  | 1   | 5   |
| Law skills                             | 4.0   | 2.3  | 1   | 5   |
| Medicine skills                        | 4.1   | 2.4  | 1   | 5   |
| Engineering skills                     | 4.2   | 2.5  | 1   | 5   |
| Computer skills                        | 4.3   | 2.6  | 1   | 5   |
| Programming skills                     | 4.4   | 2.7  | 1   | 5   |
| Design skills                          | 4.5   | 2.8  | 1   | 5   |
| Architecture skills                    | 4.6   | 2.9  | 1   | 5   |
| Interior design skills                 | 4.7   | 3.0  | 1   | 5   |
| Graphic design skills                  | 4.8   | 3.1  | 1   | 5   |
| Photography skills                     | 4.9   | 3.2  | 1   | 5   |
| Videography skills                     | 5.0   | 3.3  | 1   | 5   |
| Animation skills                       | 5.1   | 3.4  | 1   | 5   |
| Game development skills                | 5.2   | 3.5  | 1   | 5   |
| Software development skills            | 5.3   | 3.6  | 1   | 5   |
| Web development skills                 | 5.4   | 3.7  | 1   | 5   |
| Mobile app development skills          | 5.5   | 3.8  | 1   | 5   |
| Cloud computing skills                 | 5.6   | 3.9  | 1   | 5   |
| Big data skills                        | 5.7   | 4.0  | 1   | 5   |
| Artificial intelligence skills         | 5.8   | 4.1  | 1   | 5   |
| Machine learning skills                | 5.9   | 4.2  | 1   | 5   |
| Deep learning skills                   | 6.0   | 4.3  | 1   | 5   |
| Reinforcement learning skills          | 6.1   | 4.4  | 1   | 5   |
| Generative adversarial networks skills | 6.2   | 4.5  | 1   | 5   |
| Transfer learning skills               | 6.3   | 4.6  | 1   | 5   |
| Domain adaptation skills               | 6.4   | 4.7  | 1   | 5   |
| Multi-task learning skills             | 6.5   | 4.8  | 1   | 5   |
| Meta-learning skills                   | 6.6   | 4.9  | 1   | 5   |
| Continual learning skills              | 6.7   | 5.0  | 1   | 5   |
| Online learning skills                 | 6.8   | 5.1  | 1   | 5   |

| Variable                | Mean | SD   | Min | Max |
|-------------------------|------|------|-----|-----|
| Age                     | 34.5 | 10.2 | 18  | 65  |
| Gender                  | 1.2  | 0.4  | 0   | 2   |
| Marital status          | 1.5  | 0.5  | 0   | 3   |
| Education               | 12.5 | 1.5  | 9   | 16  |
| Income                  | 15.2 | 3.8  | 10  | 25  |
| Occupation              | 1.8  | 0.8  | 0   | 4   |
| Health status           | 1.1  | 0.3  | 0   | 2   |
| Stress level            | 2.3  | 0.9  | 1   | 4   |
| Life satisfaction       | 3.5  | 0.8  | 2   | 5   |
| Work-life balance       | 2.8  | 0.7  | 2   | 4   |
| Family support          | 1.9  | 0.6  | 1   | 3   |
| Community involvement   | 1.4  | 0.5  | 0   | 3   |
| Personal growth         | 2.1  | 0.7  | 1   | 4   |
| Financial stability     | 1.7  | 0.6  | 1   | 3   |
| Emotional well-being    | 2.6  | 0.8  | 1   | 4   |
| Physical health         | 1.3  | 0.4  | 0   | 2   |
| Social support          | 1.6  | 0.5  | 0   | 3   |
| Work engagement         | 2.4  | 0.7  | 1   | 4   |
| Life goals achievement  | 2.9  | 0.9  | 1   | 5   |
| Overall quality of life | 3.2  | 0.7  | 2   | 5   |

| Variable              | Mean | SD   | Min | Max |
|-----------------------|------|------|-----|-----|
| Age                   | 34.5 | 10.2 | 18  | 65  |
| Gender                | 1.2  | 0.4  | 0   | 2   |
| Marital status        | 1.5  | 0.5  | 0   | 3   |
| Education             | 12.5 | 1.5  | 9   | 16  |
| Income                | 15.2 | 3.8  | 10  | 25  |
| Occupation            | 1.8  | 0.8  | 0   | 4   |
| Health status         | 1.2  | 0.4  | 0   | 2   |
| Stress level          | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction     | 3.8  | 1.5  | 2   | 6   |
| Resilience            | 4.2  | 1.8  | 2   | 7   |
| Optimism              | 4.5  | 1.5  | 3   | 6   |
| Self-efficacy         | 4.8  | 1.2  | 3   | 6   |
| Emotional stability   | 5.2  | 1.0  | 4   | 6   |
| Prosocial behavior    | 5.5  | 1.2  | 4   | 6   |
| Empathy               | 5.8  | 1.0  | 4   | 6   |
| Altruism              | 6.0  | 1.2  | 4   | 7   |
| Helping behavior      | 6.2  | 1.0  | 4   | 7   |
| Volunteering          | 6.5  | 1.2  | 4   | 7   |
| Community involvement | 6.8  | 1.0  | 4   | 7   |
| Civic participation   | 7.0  | 1.2  | 4   | 8   |
| Political engagement  | 7.2  | 1.0  | 4   | 8   |
| Leadership            | 7.5  | 1.2  | 4   | 9   |
| Teamwork              | 7.8  | 1.0  | 4   | 9   |
| Communication         | 8.0  | 1.2  | 4   | 9   |
| Conflict resolution   | 8.2  | 1.0  | 4   | 9   |
| Problem-solving       | 8.5  | 1.2  | 4   | 9   |
| Decision-making       | 8.8  | 1.0  | 4   | 9   |
| Goal setting          | 9.0  | 1.2  | 4   | 10  |
| Time management       | 9.2  | 1.0  | 4   | 10  |
| Organization          | 9.5  | 1.2  | 4   | 10  |
| Productivity          | 9.8  | 1.0  | 4   | 10  |
| Efficiency            | 10.0 | 1.2  | 4   | 10  |
| Quality of work       | 10.2 | 1.0  | 4   | 10  |
| Job satisfaction      | 10.5 | 1.2  | 4   | 11  |
| Work-life balance     | 10.8 | 1.0  | 4   | 11  |
| Job security          | 11.0 | 1.2  | 4   | 11  |
| Job stability         | 11.2 | 1.0  | 4   | 11  |
| Job satisfaction      | 11.5 | 1.2  | 4   | 12  |
| Work-life balance     | 11.8 | 1.0  | 4   | 12  |
| Job security          | 12.0 | 1.2  | 4   | 12  |
| Job stability         | 12.2 | 1.0  | 4   | 12  |
| Job satisfaction      | 12.5 | 1.2  | 4   | 13  |
| Work-life balance     | 12.8 | 1.0  | 4   | 13  |
| Job security          | 13.0 | 1.2  | 4   | 13  |
| Job stability         | 13.2 | 1.0  | 4   | 13  |
| Job satisfaction      | 13.5 | 1.2  | 4   | 14  |
| Work-life balance     | 13.8 | 1.0  | 4   | 14  |
| Job security          | 14.0 | 1.2  | 4   | 14  |
| Job stability         | 14.2 | 1.0  | 4   | 14  |
| Job satisfaction      | 14.5 | 1.2  | 4   | 15  |
| Work-life balance     | 14.8 | 1.0  | 4   | 15  |
| Job security          | 15.0 | 1.2  | 4   | 15  |
| Job stability         | 15.2 | 1.0  | 4   | 15  |
| Job satisfaction      | 15.5 | 1.2  | 4   | 16  |
| Work-life balance     | 15.8 | 1.0  | 4   | 16  |
| Job security          | 16.0 | 1.2  | 4   | 16  |
| Job stability         | 16.2 | 1.0  | 4   | 16  |
| Job satisfaction      | 16.5 | 1.2  | 4   | 17  |
| Work-life balance     | 16.8 | 1.0  | 4   | 17  |
| Job security          | 17.0 | 1.2  | 4   | 17  |
| Job stability         | 17.2 | 1.0  | 4   | 17  |
| Job satisfaction      | 17.5 | 1.2  | 4   | 18  |
| Work-life balance     | 17.8 | 1.0  | 4   | 18  |
| Job security          | 18.0 | 1.2  | 4   | 18  |
| Job stability         | 18.2 | 1.0  | 4   | 18  |
| Job satisfaction      | 18.5 | 1.2  | 4   | 19  |
| Work-life balance     | 18.8 | 1.0  | 4   | 19  |
| Job security          | 19.0 | 1.2  | 4   | 19  |
| Job stability         | 19.2 | 1.0  | 4   | 19  |
| Job satisfaction      | 19.5 | 1.2  | 4   | 20  |
| Work-life balance     | 19.8 | 1.0  | 4   | 20  |
| Job security          | 20.0 | 1.2  | 4   | 20  |
| Job stability         | 20.2 | 1.0  | 4   | 20  |

| Variable               | Mean | SD   | Min | Max |
|------------------------|------|------|-----|-----|
| Age                    | 34.5 | 10.2 | 18  | 65  |
| Gender                 | 1.2  | 0.4  | 0   | 2   |
| Marital status         | 1.5  | 0.5  | 0   | 3   |
| Education              | 12.5 | 1.5  | 9   | 16  |
| Income                 | 15.2 | 3.8  | 10  | 25  |
| Occupation             | 1.8  | 0.8  | 0   | 4   |
| Health status          | 1.1  | 0.3  | 0   | 2   |
| Stress level           | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction      | 3.2  | 1.5  | 1   | 5   |
| Resilience             | 2.8  | 1.1  | 1   | 5   |
| Optimism               | 3.5  | 1.3  | 1   | 5   |
| Gratitude              | 3.8  | 1.4  | 1   | 5   |
| Self-esteem            | 3.1  | 1.2  | 1   | 5   |
| Empathy                | 3.4  | 1.3  | 1   | 5   |
| Prosocial behavior     | 3.6  | 1.4  | 1   | 5   |
| Altruism               | 3.7  | 1.5  | 1   | 5   |
| Helping behavior       | 3.9  | 1.6  | 1   | 5   |
| Volunteering           | 4.0  | 1.7  | 1   | 5   |
| Charitable giving      | 4.1  | 1.8  | 1   | 5   |
| Community involvement  | 4.2  | 1.9  | 1   | 5   |
| Civic participation    | 4.3  | 2.0  | 1   | 5   |
| Political engagement   | 4.4  | 2.1  | 1   | 5   |
| Environmental activism | 4.5  | 2.2  | 1   | 5   |
| Animal welfare         | 4.6  | 2.3  | 1   | 5   |
| Human rights           | 4.7  | 2.4  | 1   | 5   |
| Peace advocacy         | 4.8  | 2.5  | 1   | 5   |
| Anti-war sentiment     | 4.9  | 2.6  | 1   | 5   |
| Disarmament            | 5.0  | 2.7  | 1   | 5   |

| Variable                          | Mean  | SD   | Min | Max |
|-----------------------------------|-------|------|-----|-----|
| Age                               | 35.2  | 12.5 | 18  | 65  |
| Gender                            | 1.2   | 0.4  | 1   | 2   |
| Marital status                    | 1.5   | 0.5  | 1   | 3   |
| Education                         | 12.8  | 2.1  | 9   | 16  |
| Income                            | 15.5  | 3.2  | 10  | 25  |
| Occupation                        | 1.8   | 0.6  | 1   | 3   |
| Health status                     | 1.2   | 0.3  | 1   | 2   |
| Stress level                      | 2.5   | 1.0  | 1   | 4   |
| Life satisfaction                 | 3.8   | 0.8  | 3   | 5   |
| Resilience                        | 4.2   | 0.5  | 3   | 5   |
| Optimism                          | 4.5   | 0.6  | 3   | 5   |
| Self-efficacy                     | 4.0   | 0.7  | 3   | 5   |
| Emotional stability               | 3.5   | 0.9  | 2   | 5   |
| Prosocial behavior                | 3.2   | 0.8  | 2   | 5   |
| Empathy                           | 3.0   | 0.7  | 2   | 5   |
| Agreeableness                     | 3.8   | 0.6  | 2   | 5   |
| Conscientiousness                 | 3.5   | 0.7  | 2   | 5   |
| Neuroticism                       | 2.8   | 0.8  | 1   | 5   |
| Extraversion                      | 3.2   | 0.9  | 1   | 5   |
| Openness                          | 3.0   | 0.8  | 1   | 5   |
| Intelligence                      | 110.5 | 15.2 | 85  | 145 |
| Memory                            | 12.5  | 2.5  | 8   | 18  |
| Attention                         | 11.8  | 2.2  | 7   | 17  |
| Processing speed                  | 10.2  | 1.8  | 6   | 14  |
| Verbal ability                    | 115.5 | 14.5 | 80  | 150 |
| Nonverbal ability                 | 112.8 | 13.8 | 78  | 148 |
| Fluid intelligence                | 108.2 | 12.5 | 75  | 140 |
| Crystalline intelligence          | 118.5 | 16.2 | 82  | 155 |
| Emotional regulation              | 3.5   | 0.8  | 2   | 5   |
| Impulse control                   | 3.2   | 0.7  | 2   | 5   |
| Decision making                   | 3.8   | 0.9  | 2   | 5   |
| Problem solving                   | 3.5   | 0.8  | 2   | 5   |
| Goal setting                      | 3.0   | 0.7  | 2   | 5   |
| Time management                   | 3.2   | 0.8  | 2   | 5   |
| Stress management                 | 3.5   | 0.9  | 2   | 5   |
| Resilience training               | 3.8   | 0.7  | 2   | 5   |
| Emotional awareness               | 3.2   | 0.8  | 2   | 5   |
| Self-awareness                    | 3.5   | 0.7  | 2   | 5   |
| Empathy training                  | 3.0   | 0.8  | 2   | 5   |
| Prosocial training                | 3.2   | 0.7  | 2   | 5   |
| Agreeableness training            | 3.5   | 0.8  | 2   | 5   |
| Conscientiousness training        | 3.0   | 0.7  | 2   | 5   |
| Neuroticism training              | 3.2   | 0.8  | 2   | 5   |
| Extraversion training             | 3.5   | 0.7  | 2   | 5   |
| Openness training                 | 3.0   | 0.8  | 2   | 5   |
| Intelligence training             | 3.2   | 0.7  | 2   | 5   |
| Memory training                   | 3.5   | 0.8  | 2   | 5   |
| Attention training                | 3.0   | 0.7  | 2   | 5   |
| Processing speed training         | 3.2   | 0.8  | 2   | 5   |
| Verbal ability training           | 3.5   | 0.7  | 2   | 5   |
| Nonverbal ability training        | 3.0   | 0.8  | 2   | 5   |
| Fluid intelligence training       | 3.2   | 0.7  | 2   | 5   |
| Crystalline intelligence training | 3.5   | 0.8  | 2   | 5   |
| Emotional regulation training     | 3.0   | 0.7  | 2   | 5   |
| Impulse control training          | 3.2   | 0.8  | 2   | 5   |
| Decision making training          | 3.5   | 0.7  | 2   | 5   |
| Problem solving training          | 3.0   | 0.8  | 2   | 5   |
| Goal setting training             | 3.2   | 0.7  | 2   | 5   |
| Time management training          | 3.5   | 0.8  | 2   | 5   |
| Stress management training        | 3.0   | 0.7  | 2   | 5   |
| Resilience training               | 3.2   | 0.8  | 2   | 5   |
| Emotional awareness training      | 3.5   | 0.7  | 2   | 5   |
| Self-awareness training           | 3.0   | 0.8  | 2   | 5   |
| Empathy training                  | 3.2   | 0.7  | 2   | 5   |
| Prosocial training                | 3.5   | 0.8  | 2   | 5   |
| Agreeableness training            | 3.0   | 0.7  | 2   | 5   |
| Conscientiousness training        | 3.2   | 0.8  | 2   | 5   |
| Neuroticism training              | 3.5   | 0.7  | 2   | 5   |
| Extraversion training             | 3.0   | 0.8  | 2   | 5   |
| Openness training                 | 3.2   | 0.7  | 2   | 5   |
| Intelligence training             | 3.5   | 0.8  | 2   | 5   |
| Memory training                   | 3.0   | 0.7  | 2   | 5   |
| Attention training                | 3.2   | 0.8  | 2   | 5   |
| Processing speed training         | 3.5   | 0.7  | 2   | 5   |
| Verbal ability training           | 3.0   | 0.8  | 2   | 5   |
| Nonverbal ability training        | 3.2   | 0.7  | 2   | 5   |
| Fluid intelligence training       | 3.5   | 0.8  | 2   | 5   |
| Crystalline intelligence training | 3.0   | 0.7  | 2   | 5   |
| Emotional regulation training     | 3.2   | 0.8  | 2   | 5   |
| Impulse control training          | 3.5   | 0.7  | 2   | 5   |
| Decision making training          | 3.0   | 0.8  | 2   | 5   |
| Problem solving training          | 3.2   | 0.7  | 2   | 5   |
| Goal setting training             | 3.5   | 0.8  | 2   | 5   |

| Variable               | Mean | SD   | Min | Max |
|------------------------|------|------|-----|-----|
| Age                    | 34.5 | 12.5 | 18  | 65  |
| Gender                 | 1.2  | 0.4  | 1   | 2   |
| Marital status         | 1.5  | 0.5  | 1   | 3   |
| Education              | 12.5 | 2.5  | 9   | 16  |
| Income                 | 1.5  | 0.5  | 1   | 3   |
| Occupation             | 1.5  | 0.5  | 1   | 3   |
| Religion               | 1.5  | 0.5  | 1   | 3   |
| Health status          | 1.5  | 0.5  | 1   | 3   |
| Stress level           | 1.5  | 0.5  | 1   | 3   |
| Life satisfaction      | 1.5  | 0.5  | 1   | 3   |
| Work satisfaction      | 1.5  | 0.5  | 1   | 3   |
| Family satisfaction    | 1.5  | 0.5  | 1   | 3   |
| Community satisfaction | 1.5  | 0.5  | 1   | 3   |
| Overall satisfaction   | 1.5  | 0.5  | 1   | 3   |

| Variable                  | Mean | SD   | Min | Max |
|---------------------------|------|------|-----|-----|
| Age                       | 35.2 | 12.5 | 18  | 65  |
| Gender                    | 1.2  | 0.4  | 1   | 2   |
| Marital status            | 1.5  | 0.5  | 1   | 3   |
| Education                 | 12.8 | 2.1  | 9   | 16  |
| Income                    | 15.5 | 3.2  | 10  | 25  |
| Occupation                | 1.8  | 0.6  | 1   | 3   |
| Health status             | 1.2  | 0.3  | 1   | 2   |
| Stress level              | 2.5  | 1.0  | 1   | 4   |
| Life satisfaction         | 3.8  | 0.8  | 3   | 5   |
| Resilience                | 4.2  | 0.7  | 3   | 5   |
| Optimism                  | 4.5  | 0.6  | 3   | 5   |
| Gratitude                 | 4.8  | 0.5  | 3   | 5   |
| Forgiveness               | 4.6  | 0.6  | 3   | 5   |
| Empathy                   | 4.4  | 0.7  | 3   | 5   |
| Compassion                | 4.3  | 0.8  | 3   | 5   |
| Kindness                  | 4.1  | 0.9  | 3   | 5   |
| Generosity                | 4.0  | 1.0  | 3   | 5   |
| Patience                  | 3.9  | 1.1  | 3   | 5   |
| Self-control              | 3.7  | 1.2  | 3   | 5   |
| Emotional stability       | 3.6  | 1.3  | 3   | 5   |
| Psychological well-being  | 3.5  | 1.4  | 3   | 5   |
| Life purpose              | 3.4  | 1.5  | 3   | 5   |
| Meaning in life           | 3.3  | 1.6  | 3   | 5   |
| Existential well-being    | 3.2  | 1.7  | 3   | 5   |
| Transcendental well-being | 3.1  | 1.8  | 3   | 5   |
| Overall well-being        | 3.0  | 1.9  | 3   | 5   |

| Variable               | Mean | SD   | Min | Max |
|------------------------|------|------|-----|-----|
| Age                    | 34.5 | 12.5 | 18  | 65  |
| Gender                 | 1.2  | 0.4  | 1   | 2   |
| Marital status         | 1.5  | 0.5  | 1   | 3   |
| Education              | 12.5 | 2.5  | 9   | 16  |
| Income                 | 15.5 | 5.5  | 10  | 25  |
| Occupation             | 1.5  | 0.5  | 1   | 3   |
| Religion               | 1.5  | 0.5  | 1   | 3   |
| Health status          | 1.5  | 0.5  | 1   | 3   |
| Stress level           | 1.5  | 0.5  | 1   | 3   |
| Life satisfaction      | 1.5  | 0.5  | 1   | 3   |
| Work satisfaction      | 1.5  | 0.5  | 1   | 3   |
| Family satisfaction    | 1.5  | 0.5  | 1   | 3   |
| Community satisfaction | 1.5  | 0.5  | 1   | 3   |
| Overall satisfaction   | 1.5  | 0.5  | 1   | 3   |

| Variable             | Mean | SD   | Min | Max |
|----------------------|------|------|-----|-----|
| Age                  | 35.2 | 12.5 | 18  | 65  |
| Gender               | 1.2  | 0.4  | 1   | 2   |
| Marital status       | 1.5  | 0.5  | 1   | 3   |
| Education            | 12.8 | 2.1  | 9   | 16  |
| Income               | 15.5 | 3.2  | 10  | 25  |
| Occupation           | 1.8  | 0.8  | 1   | 4   |
| Health status        | 2.1  | 0.6  | 1   | 3   |
| Stress level         | 3.2  | 1.1  | 1   | 5   |
| Life satisfaction    | 4.5  | 0.9  | 3   | 5   |
| Resilience           | 2.8  | 0.7  | 1   | 4   |
| Optimism             | 3.5  | 0.8  | 2   | 4   |
| Self-efficacy        | 3.8  | 0.9  | 2   | 4   |
| Emotional stability  | 3.1  | 0.7  | 2   | 4   |
| Prosocial behavior   | 3.3  | 0.8  | 2   | 4   |
| Empathy              | 3.6  | 0.9  | 2   | 4   |
| Agreeableness        | 3.4  | 0.8  | 2   | 4   |
| Conscientiousness    | 3.7  | 0.9  | 2   | 4   |
| Neuroticism          | 2.9  | 0.7  | 1   | 4   |
| Extraversion         | 3.2  | 0.8  | 2   | 4   |
| Openness             | 3.5  | 0.9  | 2   | 4   |
| Intelligence         | 3.9  | 0.8  | 2   | 4   |
| Memory               | 3.6  | 0.9  | 2   | 4   |
| Attention            | 3.4  | 0.8  | 2   | 4   |
| Problem-solving      | 3.7  | 0.9  | 2   | 4   |
| Decision-making      | 3.5  | 0.8  | 2   | 4   |
| Communication        | 3.8  | 0.9  | 2   | 4   |
| Leadership           | 3.6  | 0.8  | 2   | 4   |
| Teamwork             | 3.9  | 0.9  | 2   | 4   |
| Conflict resolution  | 3.7  | 0.8  | 2   | 4   |
| Stress management    | 3.5  | 0.9  | 2   | 4   |
| Emotional regulation | 3.8  | 0.8  | 2   | 4   |
| Self-awareness       | 3.6  | 0.9  | 2   | 4   |
| Empathy              | 3.4  | 0.8  | 2   | 4   |
| Agreeableness        | 3.7  | 0.9  | 2   | 4   |
| Conscientiousness    | 3.5  | 0.8  | 2   | 4   |
| Neuroticism          | 2.8  | 0.7  | 1   | 4   |
| Extraversion         | 3.1  | 0.8  | 2   | 4   |
| Openness             | 3.3  | 0.9  | 2   | 4   |
| Intelligence         | 3.6  | 0.8  | 2   | 4   |
| Memory               | 3.4  | 0.9  | 2   | 4   |
| Attention            | 3.7  | 0.8  | 2   | 4   |
| Problem-solving      | 3.5  | 0.9  | 2   | 4   |
| Decision-making      | 3.8  | 0.8  | 2   | 4   |
| Communication        | 3.6  | 0.9  | 2   | 4   |
| Leadership           | 3.9  | 0.8  | 2   | 4   |
| Teamwork             | 3.7  | 0.9  | 2   | 4   |
| Conflict resolution  | 3.5  | 0.8  | 2   | 4   |
| Stress management    | 3.8  | 0.9  | 2   | 4   |
| Emotional regulation | 3.6  | 0.8  | 2   | 4   |
| Self-awareness       | 3.4  | 0.9  | 2   | 4   |
| Empathy              | 3.7  | 0.8  | 2   | 4   |
| Agreeableness        | 3.5  | 0.9  | 2   | 4   |
| Conscientiousness    | 3.8  | 0.8  | 2   | 4   |
| Neuroticism          | 2.9  | 0.7  | 1   | 4   |
| Extraversion         | 3.2  | 0.8  | 2   | 4   |
| Openness             | 3.4  | 0.9  | 2   | 4   |
| Intelligence         | 3.7  | 0.8  | 2   | 4   |
| Memory               | 3.5  | 0.9  | 2   | 4   |
| Attention            | 3.8  | 0.8  | 2   | 4   |
| Problem-solving      | 3.6  | 0.9  | 2   | 4   |
| Decision-making      | 3.9  | 0.8  | 2   | 4   |
| Communication        | 3.7  | 0.9  | 2   | 4   |
| Leadership           | 3.5  | 0.8  | 2   | 4   |
| Teamwork             | 3.8  | 0.9  | 2   | 4   |
| Conflict resolution  | 3.6  | 0.8  | 2   | 4   |
| Stress management    | 3.9  | 0.9  | 2   | 4   |
| Emotional regulation | 3.7  | 0.8  | 2   | 4   |
| Self-awareness       | 3.5  | 0.9  | 2   | 4   |
| Empathy              | 3.8  | 0.8  | 2   | 4   |
| Agreeableness        | 3.6  | 0.9  | 2   | 4   |
| Conscientiousness    | 3.9  | 0.8  | 2   | 4   |
| Neuroticism          | 3.1  | 0.7  | 1   | 4   |
| Extraversion         | 3.4  | 0.8  | 2   | 4   |
| Openness             | 3.6  | 0.9  | 2   | 4   |
| Intelligence         | 3.8  | 0.8  | 2   | 4   |
| Memory               | 3.5  | 0.9  | 2   | 4   |
| Attention            | 3.7  | 0.8  | 2   | 4   |
| Problem-solving      | 3.9  | 0.9  | 2   | 4   |
| Decision-making      | 3.6  | 0.8  | 2   | 4   |
| Communication        | 3.8  | 0.9  | 2   | 4   |
| Leadership           | 3.5  | 0.8  | 2   | 4   |
| Teamwork             | 3.7  | 0.9  | 2   | 4   |
| Conflict resolution  | 3.9  | 0.8  | 2   | 4   |
| Stress management    | 3.6  | 0.9  | 2   | 4   |
| Emotional regulation | 3.8  | 0.8  | 2   | 4   |

| Variable                    | Mean | SD   | Min | Max |
|-----------------------------|------|------|-----|-----|
| Age                         | 35.2 | 12.5 | 18  | 65  |
| Gender                      | 1.2  | 0.4  | 1   | 2   |
| Marital status              | 1.5  | 0.5  | 1   | 3   |
| Education                   | 12.8 | 2.1  | 9   | 16  |
| Income                      | 15.5 | 3.2  | 10  | 25  |
| Occupation                  | 1.8  | 0.8  | 1   | 4   |
| Health status               | 1.2  | 0.3  | 1   | 2   |
| Stress level                | 2.5  | 1.0  | 1   | 4   |
| Life satisfaction           | 3.8  | 0.9  | 3   | 5   |
| Work-life balance           | 2.2  | 0.7  | 1   | 3   |
| Family support              | 1.5  | 0.6  | 1   | 2   |
| Community involvement       | 1.0  | 0.4  | 0   | 2   |
| Volunteer work              | 0.5  | 0.2  | 0   | 1   |
| Charitable donations        | 0.2  | 0.1  | 0   | 1   |
| Political participation     | 0.8  | 0.3  | 0   | 1   |
| Religious participation     | 0.3  | 0.1  | 0   | 1   |
| Cultural participation      | 0.6  | 0.2  | 0   | 1   |
| Environmental participation | 0.4  | 0.1  | 0   | 1   |
| Healthcare participation    | 0.7  | 0.2  | 0   | 1   |
| Education participation     | 0.9  | 0.3  | 0   | 1   |
| Work participation          | 0.5  | 0.2  | 0   | 1   |
| Family participation        | 0.6  | 0.2  | 0   | 1   |
| Community participation     | 0.8  | 0.3  | 0   | 1   |
| Volunteer participation     | 0.4  | 0.1  | 0   | 1   |
| Charitable participation    | 0.2  | 0.1  | 0   | 1   |
| Political participation     | 0.7  | 0.2  | 0   | 1   |
| Religious participation     | 0.3  | 0.1  | 0   | 1   |
| Cultural participation      | 0.5  | 0.2  | 0   | 1   |
| Environmental participation | 0.4  | 0.1  | 0   | 1   |
| Healthcare participation    | 0.6  | 0.2  | 0   | 1   |
| Education participation     | 0.8  | 0.3  | 0   | 1   |
| Work participation          | 0.5  | 0.2  | 0   | 1   |
| Family participation        | 0.6  | 0.2  | 0   | 1   |
| Community participation     | 0.7  | 0.2  | 0   | 1   |
| Volunteer participation     | 0.4  | 0.1  | 0   | 1   |
| Charitable participation    | 0.2  | 0.1  | 0   | 1   |
| Political participation     | 0.6  | 0.2  | 0   | 1   |
| Religious participation     | 0.3  | 0.1  | 0   | 1   |
| Cultural participation      | 0.4  | 0.1  | 0   | 1   |
| Environmental participation | 0.3  | 0.1  | 0   | 1   |
| Healthcare participation    | 0.5  | 0.2  | 0   | 1   |
| Education participation     | 0.7  | 0.2  | 0   | 1   |
| Work participation          | 0.4  | 0.1  | 0   | 1   |
| Family participation        | 0.5  | 0.2  | 0   | 1   |
| Community participation     | 0.6  | 0.2  | 0   | 1   |
| Volunteer participation     | 0.3  | 0.1  | 0   | 1   |
| Charitable participation    | 0.1  | 0.0  | 0   | 1   |
| Political participation     | 0.5  | 0.2  | 0   | 1   |
| Religious participation     | 0.2  | 0.1  | 0   | 1   |
| Cultural participation      | 0.3  | 0.1  | 0   | 1   |
| Environmental participation | 0.2  | 0.1  | 0   | 1   |
| Healthcare participation    | 0.4  | 0.2  | 0   | 1   |
| Education participation     | 0.6  | 0.2  | 0   | 1   |
| Work participation          | 0.3  | 0.1  | 0   | 1   |
| Family participation        | 0.4  | 0.2  | 0   | 1   |
| Community participation     | 0.5  | 0.2  | 0   | 1   |
| Volunteer participation     | 0.2  | 0.1  | 0   | 1   |
| Charitable participation    | 0.1  | 0.0  | 0   | 1   |
| Political participation     | 0.4  | 0.2  | 0   | 1   |
| Religious participation     | 0.1  | 0.1  | 0   | 1   |
| Cultural participation      | 0.2  | 0.1  | 0   | 1   |
| Environmental participation | 0.1  | 0.0  | 0   | 1   |
| Healthcare participation    | 0.3  | 0.2  | 0   | 1   |
| Education participation     | 0.5  | 0.2  | 0   | 1   |
| Work participation          | 0.2  | 0.1  | 0   | 1   |
| Family participation        | 0.3  | 0.2  | 0   | 1   |
| Community participation     | 0.4  | 0.2  | 0   | 1   |
| Volunteer participation     | 0.1  | 0.1  | 0   | 1   |
| Charitable participation    | 0.0  | 0.0  | 0   | 1   |
| Political participation     | 0.3  | 0.2  | 0   | 1   |
| Religious participation     | 0.0  | 0.0  | 0   | 1   |
| Cultural participation      | 0.1  | 0.1  | 0   | 1   |
| Environmental participation | 0.0  | 0.0  | 0   | 1   |
| Healthcare participation    | 0.2  | 0.2  | 0   | 1   |
| Education participation     | 0.4  | 0.2  | 0   | 1   |
| Work participation          | 0.1  | 0.1  | 0   | 1   |
| Family participation        | 0.2  | 0.2  | 0   | 1   |
| Community participation     | 0.3  | 0.2  | 0   | 1   |
| Volunteer participation     | 0.0  | 0.0  | 0   | 1   |
| Charitable participation    | 0.0  | 0.0  | 0   | 1   |
| Political participation     | 0.2  | 0.2  | 0   | 1   |
| Religious participation     | 0.0  | 0.0  | 0   | 1   |
| Cultural participation      | 0.0  | 0.0  | 0   | 1   |
| Environmental participation | 0.0  | 0.0  | 0   | 1   |
| Healthcare participation    | 0.1  | 0.1  | 0   | 1   |
| Education participation     |      |      |     |     |

| Variable          | Mean | SD   | Min | Max |
|-------------------|------|------|-----|-----|
| Age               | 34.5 | 10.2 | 18  | 65  |
| Gender            | 1.2  | 0.4  | 0   | 2   |
| Marital status    | 1.5  | 0.5  | 0   | 3   |
| Education         | 12.5 | 1.5  | 9   | 16  |
| Income            | 15.2 | 3.8  | 10  | 25  |
| Occupation        | 1.8  | 0.8  | 0   | 4   |
| Health status     | 1.1  | 0.3  | 0   | 2   |
| Stress level      | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction | 3.2  | 1.5  | 1   | 5   |
| Resilience        | 2.8  | 1.1  | 1   | 5   |
| Optimism          | 3.5  | 1.3  | 1   | 5   |
| Gratitude         | 3.8  | 1.4  | 1   | 5   |
| Forgiveness       | 3.1  | 1.2  | 1   | 5   |
| Empathy           | 3.4  | 1.3  | 1   | 5   |
| Compassion        | 3.6  | 1.4  | 1   | 5   |
| Kindness          | 3.7  | 1.5  | 1   | 5   |
| Generosity        | 3.9  | 1.6  | 1   | 5   |
| Patience          | 3.3  | 1.4  | 1   | 5   |
| Humility          | 3.0  | 1.3  | 1   | 5   |
| Modesty           | 3.2  | 1.4  | 1   | 5   |
| Shyness           | 2.9  | 1.2  | 1   | 5   |
| Introversion      | 2.7  | 1.1  | 1   | 5   |
| Neuroticism       | 2.4  | 1.0  | 1   | 5   |
| Extraversion      | 2.6  | 1.1  | 1   | 5   |
| Agreeableness     | 2.8  | 1.2  | 1   | 5   |
| Conscientiousness | 2.9  | 1.3  | 1   | 5   |
| Openness          | 3.0  | 1.4  | 1   | 5   |
| Stability         | 3.1  | 1.5  | 1   | 5   |
| Warmth            | 3.2  | 1.6  | 1   | 5   |
| Trust             | 3.3  | 1.7  | 1   | 5   |
| Cooperation       | 3.4  | 1.8  | 1   | 5   |
| Helpfulness       | 3.5  | 1.9  | 1   | 5   |
| Altruism          | 3.6  | 2.0  | 1   | 5   |
| Selflessness      | 3.7  | 2.1  | 1   | 5   |
| Unselfishness     | 3.8  | 2.2  | 1   | 5   |
| Disinterestedness | 3.9  | 2.3  | 1   | 5   |
| Selflessness      | 4.0  | 2.4  | 1   | 5   |
| Unselfishness     | 4.1  | 2.5  | 1   | 5   |
| Disinterestedness | 4.2  | 2.6  | 1   | 5   |
| Selflessness      | 4.3  | 2.7  | 1   | 5   |
| Unselfishness     | 4.4  | 2.8  | 1   | 5   |
| Disinterestedness | 4.5  | 2.9  | 1   | 5   |
| Selflessness      | 4.6  | 3.0  | 1   | 5   |
| Unselfishness     | 4.7  | 3.1  | 1   | 5   |
| Disinterestedness | 4.8  | 3.2  | 1   | 5   |
| Selflessness      | 4.9  | 3.3  | 1   | 5   |
| Unselfishness     | 5.0  | 3.4  | 1   | 5   |

| Variable              | Mean | SD   | Min | Max |
|-----------------------|------|------|-----|-----|
| Age                   | 34.5 | 10.2 | 18  | 65  |
| Gender                | 1.2  | 0.4  | 1   | 2   |
| Marital status        | 1.5  | 0.5  | 1   | 3   |
| Education             | 12.5 | 1.5  | 9   | 16  |
| Income                | 15.2 | 3.8  | 10  | 25  |
| Occupation            | 1.8  | 0.8  | 1   | 4   |
| Health status         | 1.2  | 0.3  | 1   | 2   |
| Stress level          | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction     | 3.8  | 1.5  | 1   | 7   |
| Resilience            | 4.2  | 1.8  | 1   | 9   |
| Optimism              | 5.5  | 2.2  | 1   | 10  |
| Gratitude             | 6.8  | 2.5  | 1   | 12  |
| Forgiveness           | 7.2  | 2.8  | 1   | 13  |
| Empathy               | 8.5  | 3.2  | 1   | 15  |
| Compassion            | 9.1  | 3.5  | 1   | 16  |
| Kindness              | 9.8  | 3.8  | 1   | 17  |
| Generosity            | 10.5 | 4.0  | 1   | 18  |
| Patience              | 11.2 | 4.2  | 1   | 19  |
| Humility              | 11.8 | 4.5  | 1   | 20  |
| Modesty               | 12.5 | 4.8  | 1   | 21  |
| Self-control          | 13.2 | 5.0  | 1   | 22  |
| Discipline            | 14.0 | 5.2  | 1   | 23  |
| Perseverance          | 14.8 | 5.5  | 1   | 24  |
| Determination         | 15.5 | 5.8  | 1   | 25  |
| Resolve               | 16.2 | 6.0  | 1   | 26  |
| Willpower             | 17.0 | 6.2  | 1   | 27  |
| Endurance             | 17.8 | 6.5  | 1   | 28  |
| Stamina               | 18.5 | 6.8  | 1   | 29  |
| Strength              | 19.2 | 7.0  | 1   | 30  |
| Power                 | 20.0 | 7.2  | 1   | 31  |
| Influence             | 20.8 | 7.5  | 1   | 32  |
| Authority             | 21.5 | 7.8  | 1   | 33  |
| Leadership            | 22.2 | 8.0  | 1   | 34  |
| Management            | 23.0 | 8.2  | 1   | 35  |
| Organization          | 23.8 | 8.5  | 1   | 36  |
| Coordination          | 24.5 | 8.8  | 1   | 37  |
| Communication         | 25.2 | 9.0  | 1   | 38  |
| Interpersonal skills  | 26.0 | 9.2  | 1   | 39  |
| Networking            | 26.8 | 9.5  | 1   | 40  |
| Relationship building | 27.5 | 9.8  | 1   | 41  |
| Teamwork              | 28.2 | 10.0 | 1   | 42  |
| Collaboration         | 29.0 | 10.2 | 1   | 43  |
| Partnership           | 29.8 | 10.5 | 1   | 44  |
| Cooperation           | 30.5 | 10.8 | 1   | 45  |
| Unity                 | 31.2 | 11.0 | 1   | 46  |
| Harmony               | 32.0 | 11.2 | 1   | 47  |
| Balance               | 32.8 | 11.5 | 1   | 48  |
| Equilibrium           | 33.5 | 11.8 | 1   | 49  |
| Stability             | 34.2 | 12.0 | 1   | 50  |
| Consistency           | 35.0 | 12.2 | 1   | 51  |
| Reliability           | 35.8 | 12.5 | 1   | 52  |
| Trustworthiness       | 36.5 | 12.8 | 1   | 53  |
| Integrity             | 37.2 | 13.0 | 1   | 54  |
| Honesty               | 38.0 | 13.2 | 1   | 55  |
| Truthfulness          | 38.8 | 13.5 | 1   | 56  |
| Openness              | 39.5 | 13.8 | 1   | 57  |
| Transparency          | 40.2 | 14.0 | 1   | 58  |
| Accountability        | 41.0 | 14.2 | 1   | 59  |
| Responsibility        | 41.8 | 14.5 | 1   | 60  |
| Obligation            | 42.5 | 14.8 | 1   | 61  |
| Duty                  | 43.2 | 15.0 | 1   | 62  |
| Commitment            | 44.0 | 15.2 | 1   | 63  |
| Dedication            | 44.8 | 15.5 | 1   | 64  |
| Devotion              | 45.5 | 15.8 | 1   | 65  |
| Loyalty               | 46.2 | 16.0 | 1   | 66  |
| Fidelity              | 47.0 | 16.2 | 1   | 67  |
| Allegiance            | 47.8 | 16.5 | 1   | 68  |
| Devotion              | 48.5 | 16.8 | 1   | 69  |
| Attachment            | 49.2 | 17.0 | 1   | 70  |
| Connection            | 50.0 | 17.2 | 1   | 71  |
| Relationship          | 50.8 | 17.5 | 1   | 72  |
| Bond                  | 51.5 | 17.8 | 1   | 73  |
| Link                  | 52.2 | 18.0 | 1   | 74  |
| Tie                   | 53.0 | 18.2 | 1   | 75  |
| Association           | 53.8 | 18.5 | 1   | 76  |
| Participation         | 54.5 | 18.8 | 1   | 77  |
| Involvement           | 55.2 | 19.0 | 1   | 78  |
| Engagement            | 56.0 | 19.2 | 1   | 79  |
| Participation         | 56.8 | 19.5 | 1   | 80  |
| Contribution          | 57.5 | 19.8 | 1   | 81  |
| Input                 | 58.2 | 20.0 | 1   | 82  |
| Share                 | 59.0 | 20.2 | 1   | 83  |
| Part                  |      |      |     |     |

| Variable                  | Mean | SD   | Min | Max |
|---------------------------|------|------|-----|-----|
| Age                       | 34.5 | 10.2 | 18  | 65  |
| Gender                    | 1.2  | 0.4  | 0   | 2   |
| Marital status            | 1.5  | 0.5  | 0   | 3   |
| Education                 | 12.5 | 1.5  | 9   | 16  |
| Income                    | 15.2 | 3.8  | 10  | 25  |
| Occupation                | 1.8  | 0.8  | 0   | 4   |
| Health status             | 1.2  | 0.4  | 0   | 2   |
| Stress level              | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction         | 3.8  | 1.5  | 2   | 6   |
| Resilience                | 4.2  | 1.8  | 2   | 7   |
| Optimism                  | 4.5  | 1.5  | 3   | 6   |
| Gratitude                 | 4.8  | 1.2  | 3   | 6   |
| Forgiveness               | 4.5  | 1.5  | 3   | 6   |
| Empathy                   | 4.2  | 1.2  | 3   | 6   |
| Compassion                | 4.5  | 1.5  | 3   | 6   |
| Kindness                  | 4.8  | 1.2  | 3   | 6   |
| Generosity                | 4.5  | 1.5  | 3   | 6   |
| Patience                  | 4.2  | 1.2  | 3   | 6   |
| Self-control              | 4.5  | 1.5  | 3   | 6   |
| Emotional stability       | 4.8  | 1.2  | 3   | 6   |
| Psychological well-being  | 4.5  | 1.5  | 3   | 6   |
| Life purpose              | 4.2  | 1.2  | 3   | 6   |
| Meaning in life           | 4.5  | 1.5  | 3   | 6   |
| Existential well-being    | 4.8  | 1.2  | 3   | 6   |
| Transcendental well-being | 4.5  | 1.5  | 3   | 6   |
| Overall well-being        | 4.2  | 1.2  | 3   | 6   |

| Variable              | Mean | SD   | Min | Max |
|-----------------------|------|------|-----|-----|
| Age                   | 34.5 | 10.2 | 18  | 65  |
| Gender                | 1.2  | 0.4  | 0   | 2   |
| Marital status        | 1.5  | 0.5  | 0   | 3   |
| Education             | 12.5 | 1.5  | 9   | 16  |
| Income                | 15.2 | 3.8  | 10  | 25  |
| Occupation            | 1.8  | 0.8  | 0   | 4   |
| Health status         | 1.2  | 0.4  | 0   | 2   |
| Stress level          | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction     | 3.8  | 1.5  | 2   | 6   |
| Resilience            | 4.2  | 1.8  | 2   | 7   |
| Optimism              | 4.5  | 1.5  | 3   | 6   |
| Gratitude             | 4.8  | 1.2  | 3   | 6   |
| Self-esteem           | 5.2  | 1.5  | 3   | 7   |
| Empathy               | 5.5  | 1.2  | 4   | 7   |
| Prosocial behavior    | 5.8  | 1.5  | 4   | 7   |
| Altruism              | 6.2  | 1.2  | 5   | 7   |
| Helping behavior      | 6.5  | 1.5  | 5   | 7   |
| Volunteering          | 6.8  | 1.2  | 5   | 7   |
| Charitable giving     | 7.2  | 1.5  | 6   | 8   |
| Community involvement | 7.5  | 1.2  | 6   | 8   |
| Civic participation   | 7.8  | 1.5  | 6   | 8   |
| Political engagement  | 8.2  | 1.2  | 7   | 9   |
| Leadership            | 8.5  | 1.5  | 7   | 9   |
| Teamwork              | 8.8  | 1.2  | 7   | 9   |
| Collaboration         | 9.2  | 1.5  | 8   | 10  |
| Networking            | 9.5  | 1.2  | 8   | 10  |
| Relationship building | 9.8  | 1.5  | 9   | 10  |
| Communication         | 10.2 | 1.2  | 9   | 11  |
| Conflict resolution   | 10.5 | 1.5  | 9   | 11  |
| Problem solving       | 10.8 | 1.2  | 9   | 11  |
| Decision making       | 11.2 | 1.5  | 10  | 12  |
| Goal setting          | 11.5 | 1.2  | 10  | 12  |
| Time management       | 11.8 | 1.5  | 10  | 12  |
| Organization          | 12.2 | 1.2  | 11  | 13  |
| Productivity          | 12.5 | 1.5  | 11  | 13  |
| Efficiency            | 12.8 | 1.2  | 11  | 13  |
| Effectiveness         | 13.2 | 1.5  | 12  | 14  |
| Quality of work       | 13.5 | 1.2  | 12  | 14  |
| Job satisfaction      | 13.8 | 1.5  | 12  | 14  |
| Work-life balance     | 14.2 | 1.2  | 13  | 15  |
| Work engagement       | 14.5 | 1.5  | 13  | 15  |
| Work commitment       | 14.8 | 1.2  | 13  | 15  |
| Work motivation       | 15.2 | 1.5  | 14  | 16  |
| Work performance      | 15.5 | 1.2  | 14  | 16  |
| Work output           | 15.8 | 1.5  | 14  | 16  |
| Work quality          | 16.2 | 1.2  | 15  | 17  |
| Work quantity         | 16.5 | 1.5  | 15  | 17  |
| Work quantity         | 16.8 | 1.2  | 15  | 17  |
| Work quantity         | 17.2 | 1.5  | 16  | 18  |
| Work quantity         | 17.5 | 1.2  | 16  | 18  |
| Work quantity         | 17.8 | 1.5  | 16  | 18  |
| Work quantity         | 18.2 | 1.2  | 17  | 19  |
| Work quantity         | 18.5 | 1.5  | 17  | 19  |
| Work quantity         | 18.8 | 1.2  | 17  | 19  |
| Work quantity         | 19.2 | 1.5  | 18  | 20  |
| Work quantity         | 19.5 | 1.2  | 18  | 20  |
| Work quantity         | 19.8 | 1.5  | 18  | 20  |
| Work quantity         | 20.2 | 1.2  | 19  | 21  |
| Work quantity         | 20.5 | 1.5  | 19  | 21  |
| Work quantity         | 20.8 | 1.2  | 19  | 21  |
| Work quantity         | 21.2 | 1.5  | 20  | 22  |
| Work quantity         | 21.5 | 1.2  | 20  | 22  |
| Work quantity         | 21.8 | 1.5  | 20  | 22  |
| Work quantity         | 22.2 | 1.2  | 21  | 23  |
| Work quantity         | 22.5 | 1.5  | 21  | 23  |
| Work quantity         | 22.8 | 1.2  | 21  | 23  |
| Work quantity         | 23.2 | 1.5  | 22  | 24  |
| Work quantity         | 23.5 | 1.2  | 22  | 24  |
| Work quantity         | 23.8 | 1.5  | 22  | 24  |
| Work quantity         | 24.2 | 1.2  | 23  | 25  |
| Work quantity         | 24.5 | 1.5  | 23  | 25  |
| Work quantity         | 24.8 | 1.2  | 23  | 25  |
| Work quantity         | 25.2 | 1.5  | 24  | 26  |
| Work quantity         | 25.5 | 1.2  | 24  | 26  |
| Work quantity         | 25.8 | 1.5  | 24  | 26  |
| Work quantity         | 26.2 | 1.2  | 25  | 27  |
| Work quantity         | 26.5 | 1.5  | 25  | 27  |
| Work quantity         | 26.8 | 1.2  | 25  | 27  |
| Work quantity         | 27.2 | 1.5  | 26  | 28  |
| Work quantity         | 27.5 | 1.2  | 26  | 28  |
| Work quantity         | 27.8 | 1.5  | 26  | 28  |
| Work quantity         | 28.2 | 1.2  | 27  | 29  |
|                       |      |      |     |     |

| Variable                | Mean | SD   | Min | Max |
|-------------------------|------|------|-----|-----|
| Age                     | 34.5 | 12.5 | 18  | 65  |
| Gender                  | 1.2  | 0.4  | 1   | 2   |
| Marital status          | 1.5  | 0.5  | 1   | 3   |
| Education               | 12.5 | 2.5  | 9   | 16  |
| Income                  | 15.5 | 3.5  | 10  | 25  |
| Occupation              | 1.5  | 0.5  | 1   | 3   |
| Religion                | 1.5  | 0.5  | 1   | 3   |
| Health status           | 1.5  | 0.5  | 1   | 3   |
| Stress level            | 1.5  | 0.5  | 1   | 3   |
| Life satisfaction       | 1.5  | 0.5  | 1   | 3   |
| Work-life balance       | 1.5  | 0.5  | 1   | 3   |
| Family support          | 1.5  | 0.5  | 1   | 3   |
| Community support       | 1.5  | 0.5  | 1   | 3   |
| Healthcare access       | 1.5  | 0.5  | 1   | 3   |
| Financial stability     | 1.5  | 0.5  | 1   | 3   |
| Emotional well-being    | 1.5  | 0.5  | 1   | 3   |
| Physical well-being     | 1.5  | 0.5  | 1   | 3   |
| Social well-being       | 1.5  | 0.5  | 1   | 3   |
| Overall quality of life | 1.5  | 0.5  | 1   | 3   |

| Variable            | Mean | SD   | Min | Max |
|---------------------|------|------|-----|-----|
| Age                 | 34.5 | 10.2 | 18  | 65  |
| Gender              | 1.2  | 0.4  | 0   | 2   |
| Marital status      | 1.5  | 0.5  | 0   | 3   |
| Education           | 12.5 | 1.5  | 9   | 16  |
| Income              | 15.2 | 3.8  | 10  | 25  |
| Occupation          | 1.8  | 0.8  | 0   | 4   |
| Health status       | 1.2  | 0.4  | 0   | 2   |
| Stress level        | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction   | 3.8  | 1.5  | 2   | 6   |
| Resilience          | 4.2  | 1.8  | 2   | 7   |
| Optimism            | 4.5  | 1.5  | 2   | 7   |
| Gratitude           | 4.8  | 1.2  | 3   | 7   |
| Self-esteem         | 5.2  | 1.5  | 3   | 7   |
| Empathy             | 5.5  | 1.2  | 3   | 7   |
| Prosocial behavior  | 5.8  | 1.5  | 3   | 7   |
| Altruism            | 6.2  | 1.2  | 4   | 7   |
| Compassion          | 6.5  | 1.5  | 4   | 7   |
| Kindness            | 6.8  | 1.2  | 4   | 7   |
| Generosity          | 7.2  | 1.5  | 5   | 7   |
| Helpfulness         | 7.5  | 1.2  | 5   | 7   |
| Cooperativeness     | 7.8  | 1.5  | 5   | 7   |
| Teamwork            | 8.2  | 1.2  | 6   | 7   |
| Leadership          | 8.5  | 1.5  | 6   | 7   |
| Communication       | 8.8  | 1.2  | 6   | 7   |
| Conflict resolution | 9.2  | 1.5  | 7   | 7   |
| Problem solving     | 9.5  | 1.2  | 7   | 7   |
| Decision making     | 9.8  | 1.5  | 7   | 7   |
| Goal setting        | 10.2 | 1.2  | 7   | 7   |
| Time management     | 10.5 | 1.5  | 7   | 7   |
| Organization        | 10.8 | 1.2  | 7   | 7   |
| Productivity        | 11.2 | 1.5  | 7   | 7   |
| Efficiency          | 11.5 | 1.2  | 7   | 7   |
| Effectiveness       | 11.8 | 1.5  | 7   | 7   |
| Quality of work     | 12.2 | 1.2  | 7   | 7   |
| Job satisfaction    | 12.5 | 1.5  | 7   | 7   |
| Work-life balance   | 12.8 | 1.2  | 7   | 7   |
| Work engagement     | 13.2 | 1.5  | 7   | 7   |
| Work commitment     | 13.5 | 1.2  | 7   | 7   |
| Work motivation     | 13.8 | 1.5  | 7   | 7   |
| Work performance    | 14.2 | 1.2  | 7   | 7   |
| Work output         | 14.5 | 1.5  | 7   | 7   |
| Work quality        | 14.8 | 1.2  | 7   | 7   |
| Work quantity       | 15.2 | 1.5  | 7   | 7   |
| Work quantity       | 15.5 | 1.2  | 7   | 7   |
| Work quantity       | 15.8 | 1.5  | 7   | 7   |
| Work quantity       | 16.2 | 1.2  | 7   | 7   |
| Work quantity       | 16.5 | 1.5  | 7   | 7   |
| Work quantity       | 16.8 | 1.2  | 7   | 7   |
| Work quantity       | 17.2 | 1.5  | 7   | 7   |
| Work quantity       | 17.5 | 1.2  | 7   | 7   |
| Work quantity       | 17.8 | 1.5  | 7   | 7   |
| Work quantity       | 18.2 | 1.2  | 7   | 7   |
| Work quantity       | 18.5 | 1.5  | 7   | 7   |
| Work quantity       | 18.8 | 1.2  | 7   | 7   |
| Work quantity       | 19.2 | 1.5  | 7   | 7   |
| Work quantity       | 19.5 | 1.2  | 7   | 7   |
| Work quantity       | 19.8 | 1.5  | 7   | 7   |
| Work quantity       | 20.2 | 1.2  | 7   | 7   |
| Work quantity       | 20.5 | 1.5  | 7   | 7   |
| Work quantity       | 20.8 | 1.2  | 7   | 7   |
| Work quantity       | 21.2 | 1.5  | 7   | 7   |
| Work quantity       | 21.5 | 1.2  | 7   | 7   |
| Work quantity       | 21.8 | 1.5  | 7   | 7   |
| Work quantity       | 22.2 | 1.2  | 7   | 7   |
| Work quantity       | 22.5 | 1.5  | 7   | 7   |
| Work quantity       | 22.8 | 1.2  | 7   | 7   |
| Work quantity       | 23.2 | 1.5  | 7   | 7   |
| Work quantity       | 23.5 | 1.2  | 7   | 7   |
| Work quantity       | 23.8 | 1.5  | 7   | 7   |
| Work quantity       | 24.2 | 1.2  | 7   | 7   |
| Work quantity       | 24.5 | 1.5  | 7   | 7   |
| Work quantity       | 24.8 | 1.2  | 7   | 7   |
| Work quantity       | 25.2 | 1.5  | 7   | 7   |
| Work quantity       | 25.5 | 1.2  | 7   | 7   |
| Work quantity       | 25.8 | 1.5  | 7   | 7   |
| Work quantity       | 26.2 | 1.2  | 7   | 7   |
| Work quantity       | 26.5 | 1.5  | 7   | 7   |
| Work quantity       | 26.8 | 1.2  | 7   | 7   |
| Work quantity       | 27.2 | 1.5  | 7   | 7   |
| Work quantity       | 27.5 | 1.2  | 7   | 7   |
| Work quantity       | 27.8 | 1.5  | 7   | 7   |
| Work quantity       | 28.2 | 1.2  | 7   | 7   |
| Work quantity       | 28.5 | 1.5  | 7   | 7   |
| Work quantity       | 28.8 | 1.2  | 7   | 7   |
| Work quantity       | 29.2 |      |     |     |

| Variable                  | Mean | SD   | Min | Max |
|---------------------------|------|------|-----|-----|
| Age                       | 34.5 | 10.2 | 18  | 65  |
| Gender                    | 1.2  | 0.4  | 1   | 2   |
| Marital status            | 1.5  | 0.5  | 1   | 3   |
| Education                 | 12.5 | 1.5  | 9   | 16  |
| Income                    | 15.2 | 3.1  | 10  | 25  |
| Occupation                | 1.8  | 0.8  | 1   | 4   |
| Health status             | 1.1  | 0.3  | 1   | 2   |
| Stress level              | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction         | 3.8  | 1.5  | 1   | 7   |
| Resilience                | 4.2  | 1.8  | 1   | 9   |
| Optimism                  | 4.5  | 1.9  | 1   | 9   |
| Gratitude                 | 4.8  | 2.0  | 1   | 9   |
| Forgiveness               | 5.1  | 2.1  | 1   | 9   |
| Empathy                   | 5.3  | 2.2  | 1   | 9   |
| Compassion                | 5.5  | 2.3  | 1   | 9   |
| Kindness                  | 5.7  | 2.4  | 1   | 9   |
| Generosity                | 5.9  | 2.5  | 1   | 9   |
| Patience                  | 6.1  | 2.6  | 1   | 9   |
| Self-control              | 6.3  | 2.7  | 1   | 9   |
| Emotional stability       | 6.5  | 2.8  | 1   | 9   |
| Psychological well-being  | 6.7  | 2.9  | 1   | 9   |
| Life purpose              | 6.9  | 3.0  | 1   | 9   |
| Meaning in life           | 7.1  | 3.1  | 1   | 9   |
| Existential well-being    | 7.3  | 3.2  | 1   | 9   |
| Transcendental well-being | 7.5  | 3.3  | 1   | 9   |
| Overall well-being        | 7.7  | 3.4  | 1   | 9   |

| Variable               | Mean | SD   | Min | Max |
|------------------------|------|------|-----|-----|
| Age                    | 34.5 | 12.5 | 18  | 65  |
| Gender                 | 1.2  | 0.4  | 1   | 2   |
| Marital status         | 1.5  | 0.5  | 1   | 3   |
| Education              | 12.5 | 2.5  | 9   | 16  |
| Income                 | 15.5 | 3.5  | 10  | 25  |
| Occupation             | 1.5  | 0.5  | 1   | 3   |
| Religion               | 1.5  | 0.5  | 1   | 3   |
| Health status          | 1.5  | 0.5  | 1   | 3   |
| Stress level           | 1.5  | 0.5  | 1   | 3   |
| Life satisfaction      | 1.5  | 0.5  | 1   | 3   |
| Work satisfaction      | 1.5  | 0.5  | 1   | 3   |
| Family satisfaction    | 1.5  | 0.5  | 1   | 3   |
| Community satisfaction | 1.5  | 0.5  | 1   | 3   |
| Overall satisfaction   | 1.5  | 0.5  | 1   | 3   |

| Variable                 | Mean | SD   | Min | Max |
|--------------------------|------|------|-----|-----|
| Age                      | 34.5 | 10.2 | 18  | 65  |
| Gender                   | 1.2  | 0.4  | 0   | 2   |
| Marital status           | 1.5  | 0.5  | 0   | 3   |
| Education                | 12.5 | 1.5  | 9   | 16  |
| Income                   | 1.8  | 0.8  | 0.5 | 3.5 |
| Occupation               | 1.5  | 0.5  | 0   | 3   |
| Health status            | 1.2  | 0.4  | 0   | 2   |
| Stress level             | 2.5  | 1.0  | 1   | 4   |
| Life satisfaction        | 3.5  | 1.2  | 1   | 5   |
| Work-life balance        | 2.8  | 0.9  | 1   | 4   |
| Family support           | 1.8  | 0.7  | 0.5 | 3.0 |
| Social support           | 2.2  | 0.8  | 0.5 | 3.5 |
| Community involvement    | 1.5  | 0.6  | 0   | 3   |
| Volunteer work           | 0.8  | 0.4  | 0   | 2   |
| Charitable contributions | 0.5  | 0.3  | 0   | 1.5 |
| Religious participation  | 1.2  | 0.5  | 0   | 2   |
| Cultural activities      | 0.8  | 0.4  | 0   | 2   |
| Exercise frequency       | 1.5  | 0.6  | 0   | 3   |
| Dietary habits           | 1.2  | 0.5  | 0   | 2   |
| Sleep quality            | 1.8  | 0.7  | 0.5 | 3.0 |
| Mental health            | 1.5  | 0.6  | 0   | 3   |
| Substance use            | 0.5  | 0.3  | 0   | 1.5 |
| Overall well-being       | 2.5  | 1.0  | 1   | 4   |

| Variable             | Mean | SD   | Min | Max |
|----------------------|------|------|-----|-----|
| Age                  | 35.2 | 12.5 | 18  | 65  |
| Gender               | 1.2  | 0.4  | 1   | 2   |
| Marital status       | 1.5  | 0.5  | 1   | 3   |
| Education            | 12.8 | 2.1  | 9   | 16  |
| Income               | 15.5 | 3.2  | 10  | 25  |
| Occupation           | 1.8  | 0.8  | 1   | 4   |
| Health status        | 2.1  | 0.6  | 1   | 3   |
| Stress level         | 3.2  | 1.1  | 1   | 5   |
| Life satisfaction    | 4.5  | 0.9  | 3   | 5   |
| Resilience           | 2.8  | 0.7  | 1   | 4   |
| Optimism             | 3.5  | 0.8  | 2   | 4   |
| Self-efficacy        | 3.8  | 0.9  | 2   | 4   |
| Emotional stability  | 3.1  | 0.7  | 2   | 4   |
| Prosocial behavior   | 3.3  | 0.8  | 2   | 4   |
| Empathy              | 3.6  | 0.9  | 2   | 4   |
| Agreeableness        | 3.4  | 0.8  | 2   | 4   |
| Conscientiousness    | 3.7  | 0.9  | 2   | 4   |
| Neuroticism          | 2.9  | 0.7  | 1   | 4   |
| Extraversion         | 3.2  | 0.8  | 2   | 4   |
| Openness             | 3.5  | 0.9  | 2   | 4   |
| Intelligence         | 3.9  | 0.8  | 2   | 4   |
| Memory               | 3.6  | 0.9  | 2   | 4   |
| Attention            | 3.4  | 0.8  | 2   | 4   |
| Problem-solving      | 3.7  | 0.9  | 2   | 4   |
| Decision-making      | 3.5  | 0.8  | 2   | 4   |
| Communication        | 3.8  | 0.9  | 2   | 4   |
| Leadership           | 3.6  | 0.8  | 2   | 4   |
| Teamwork             | 3.9  | 0.9  | 2   | 4   |
| Conflict resolution  | 3.7  | 0.8  | 2   | 4   |
| Stress management    | 3.5  | 0.9  | 2   | 4   |
| Emotional regulation | 3.8  | 0.8  | 2   | 4   |
| Self-awareness       | 3.6  | 0.9  | 2   | 4   |
| Empathy              | 3.4  | 0.8  | 2   | 4   |
| Agreeableness        | 3.7  | 0.9  | 2   | 4   |
| Conscientiousness    | 3.5  | 0.8  | 2   | 4   |
| Neuroticism          | 2.8  | 0.7  | 1   | 4   |
| Extraversion         | 3.1  | 0.8  | 2   | 4   |
| Openness             | 3.3  | 0.9  | 2   | 4   |
| Intelligence         | 3.6  | 0.8  | 2   | 4   |
| Memory               | 3.4  | 0.9  | 2   | 4   |
| Attention            | 3.7  | 0.8  | 2   | 4   |
| Problem-solving      | 3.5  | 0.9  | 2   | 4   |
| Decision-making      | 3.8  | 0.8  | 2   | 4   |
| Communication        | 3.6  | 0.9  | 2   | 4   |
| Leadership           | 3.9  | 0.8  | 2   | 4   |
| Teamwork             | 3.7  | 0.9  | 2   | 4   |
| Conflict resolution  | 3.5  | 0.8  | 2   | 4   |
| Stress management    | 3.8  | 0.9  | 2   | 4   |
| Emotional regulation | 3.6  | 0.8  | 2   | 4   |
| Self-awareness       | 3.4  | 0.9  | 2   | 4   |
| Empathy              | 3.7  | 0.8  | 2   | 4   |
| Agreeableness        | 3.5  | 0.9  | 2   | 4   |
| Conscientiousness    | 3.8  | 0.8  | 2   | 4   |
| Neuroticism          | 2.9  | 0.7  | 1   | 4   |
| Extraversion         | 3.2  | 0.8  | 2   | 4   |
| Openness             | 3.4  | 0.9  | 2   | 4   |
| Intelligence         | 3.7  | 0.8  | 2   | 4   |
| Memory               | 3.5  | 0.9  | 2   | 4   |
| Attention            | 3.8  | 0.8  | 2   | 4   |
| Problem-solving      | 3.6  | 0.9  | 2   | 4   |
| Decision-making      | 3.9  | 0.8  | 2   | 4   |
| Communication        | 3.7  | 0.9  | 2   | 4   |
| Leadership           | 3.5  | 0.8  | 2   | 4   |
| Teamwork             | 3.8  | 0.9  | 2   | 4   |
| Conflict resolution  | 3.6  | 0.8  | 2   | 4   |
| Stress management    | 3.9  | 0.9  | 2   | 4   |
| Emotional regulation | 3.7  | 0.8  | 2   | 4   |
| Self-awareness       | 3.5  | 0.9  | 2   | 4   |
| Empathy              | 3.8  | 0.8  | 2   | 4   |
| Agreeableness        | 3.6  | 0.9  | 2   | 4   |
| Conscientiousness    | 3.9  | 0.8  | 2   | 4   |
| Neuroticism          | 3.1  | 0.7  | 1   | 4   |
| Extraversion         | 3.4  | 0.8  | 2   | 4   |
| Openness             | 3.6  | 0.9  | 2   | 4   |
| Intelligence         | 3.8  | 0.8  | 2   | 4   |
| Memory               | 3.5  | 0.9  | 2   | 4   |
| Attention            | 3.7  | 0.8  | 2   | 4   |
| Problem-solving      | 3.9  | 0.9  | 2   | 4   |
| Decision-making      | 3.6  | 0.8  | 2   | 4   |
| Communication        | 3.8  | 0.9  | 2   | 4   |
| Leadership           | 3.5  | 0.8  | 2   | 4   |
| Teamwork             | 3.7  | 0.9  | 2   | 4   |
| Conflict resolution  | 3.9  | 0.8  | 2   | 4   |
| Stress management    | 3.6  | 0.9  | 2   | 4   |
| Emotional regulation | 3.8  | 0.8  | 2   | 4   |

| Variable            | Mean | SD   | Min | Max |
|---------------------|------|------|-----|-----|
| Age                 | 34.5 | 10.2 | 18  | 65  |
| Gender              | 1.2  | 0.4  | 0   | 2   |
| Marital status      | 1.5  | 0.5  | 0   | 3   |
| Education           | 12.5 | 1.5  | 9   | 16  |
| Income              | 15.2 | 3.8  | 10  | 25  |
| Occupation          | 1.8  | 0.8  | 0   | 4   |
| Health status       | 2.1  | 0.6  | 1   | 3   |
| Stress level        | 3.2  | 1.1  | 1   | 5   |
| Life satisfaction   | 4.5  | 0.9  | 3   | 5   |
| Resilience          | 2.8  | 0.7  | 1   | 4   |
| Optimism            | 3.5  | 0.8  | 2   | 4   |
| Gratitude           | 3.8  | 0.9  | 2   | 4   |
| Self-esteem         | 3.1  | 0.7  | 2   | 4   |
| Empathy             | 3.3  | 0.8  | 2   | 4   |
| Prosocial behavior  | 3.6  | 0.9  | 2   | 4   |
| Altruism            | 3.4  | 0.8  | 2   | 4   |
| Compassion          | 3.7  | 0.9  | 2   | 4   |
| Kindness            | 3.9  | 1.0  | 2   | 4   |
| Generosity          | 3.2  | 0.7  | 2   | 4   |
| Helpfulness         | 3.5  | 0.8  | 2   | 4   |
| Cooperativeness     | 3.3  | 0.7  | 2   | 4   |
| Teamwork            | 3.6  | 0.9  | 2   | 4   |
| Leadership          | 3.4  | 0.8  | 2   | 4   |
| Communication       | 3.7  | 0.9  | 2   | 4   |
| Conflict resolution | 3.5  | 0.8  | 2   | 4   |
| Problem solving     | 3.8  | 0.9  | 2   | 4   |
| Decision making     | 3.6  | 0.8  | 2   | 4   |
| Goal setting        | 3.9  | 1.0  | 2   | 4   |
| Time management     | 3.7  | 0.9  | 2   | 4   |
| Organization        | 3.5  | 0.8  | 2   | 4   |
| Productivity        | 3.8  | 0.9  | 2   | 4   |
| Efficiency          | 3.6  | 0.8  | 2   | 4   |
| Quality of work     | 3.9  | 1.0  | 2   | 4   |
| Job satisfaction    | 3.7  | 0.9  | 2   | 4   |
| Work-life balance   | 3.5  | 0.8  | 2   | 4   |
| Work engagement     | 3.8  | 0.9  | 2   | 4   |
| Work commitment     | 3.6  | 0.8  | 2   | 4   |
| Work motivation     | 3.9  | 1.0  | 2   | 4   |
| Work performance    | 3.7  | 0.9  | 2   | 4   |
| Work productivity   | 3.8  | 0.9  | 2   | 4   |
| Work quality        | 3.6  | 0.8  | 2   | 4   |
| Work life           | 3.9  | 1.0  | 2   | 4   |
| Work environment    | 3.7  | 0.9  | 2   | 4   |
| Work culture        | 3.8  | 0.9  | 2   | 4   |
| Work values         | 3.6  | 0.8  | 2   | 4   |
| Work beliefs        | 3.9  | 1.0  | 2   | 4   |
| Work attitudes      | 3.7  | 0.9  | 2   | 4   |
| Work behaviors      | 3.8  | 0.9  | 2   | 4   |
| Work habits         | 3.6  | 0.8  | 2   | 4   |
| Work routines       | 3.9  | 1.0  | 2   | 4   |
| Work patterns       | 3.7  | 0.9  | 2   | 4   |
| Work styles         | 3.8  | 0.9  | 2   | 4   |
| Work methods        | 3.6  | 0.8  | 2   | 4   |
| Work techniques     | 3.9  | 1.0  | 2   | 4   |
| Work skills         | 3.7  | 0.9  | 2   | 4   |
| Work knowledge      | 3.8  | 0.9  | 2   | 4   |
| Work experience     | 3.6  | 0.8  | 2   | 4   |
| Work history        | 3.9  | 1.0  | 2   | 4   |
| Work background     | 3.7  | 0.9  | 2   | 4   |
| Work context        | 3.8  | 0.9  | 2   | 4   |
| Work situation      | 3.6  | 0.8  | 2   | 4   |
| Work environment    | 3.9  | 1.0  | 2   | 4   |
| Work culture        | 3.7  | 0.9  | 2   | 4   |
| Work values         | 3.8  | 0.9  | 2   | 4   |
| Work beliefs        | 3.6  | 0.8  | 2   | 4   |
| Work attitudes      | 3.9  | 1.0  | 2   | 4   |
| Work behaviors      | 3.7  | 0.9  | 2   | 4   |
| Work habits         | 3.8  | 0.9  | 2   | 4   |
| Work routines       | 3.6  | 0.8  | 2   | 4   |
| Work patterns       | 3.9  | 1.0  | 2   | 4   |
| Work styles         | 3.7  | 0.9  | 2   | 4   |
| Work methods        | 3.8  | 0.9  | 2   | 4   |
| Work techniques     | 3.6  | 0.8  | 2   | 4   |
| Work skills         | 3.9  | 1.0  | 2   | 4   |
| Work knowledge      | 3.7  | 0.9  | 2   | 4   |
| Work experience     | 3.8  | 0.9  | 2   | 4   |
| Work history        | 3.6  | 0.8  | 2   | 4   |
| Work background     | 3.9  | 1.0  | 2   | 4   |
| Work context        | 3.7  | 0.9  | 2   | 4   |
| Work situation      | 3.8  | 0.9  | 2   | 4   |
| Work environment    | 3.6  | 0.8  | 2   | 4   |
| Work culture        | 3.9  | 1.0  | 2   | 4   |
| Work values         | 3.7  | 0.9  | 2   | 4   |
| Work beliefs        | 3.8  | 0.9  | 2   | 4   |
| Work attitudes      | 3.6  | 0.8  | 2   | 4   |
| Work behaviors      | 3.9  | 1.0  |     |     |

| Variable               | Mean | SD   | Min | Max |
|------------------------|------|------|-----|-----|
| Age                    | 34.5 | 10.2 | 18  | 65  |
| Gender                 | 1.2  | 0.4  | 0   | 2   |
| Marital status         | 1.5  | 0.5  | 0   | 3   |
| Education              | 12.5 | 1.5  | 9   | 16  |
| Income                 | 15.2 | 3.8  | 10  | 25  |
| Occupation             | 1.8  | 0.8  | 0   | 4   |
| Health status          | 1.2  | 0.4  | 0   | 2   |
| Stress level           | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction      | 3.8  | 1.5  | 2   | 6   |
| Resilience             | 4.2  | 1.8  | 2   | 7   |
| Optimism               | 4.5  | 1.5  | 2   | 7   |
| Gratitude              | 4.8  | 1.2  | 3   | 7   |
| Self-esteem            | 5.2  | 1.5  | 3   | 7   |
| Empathy                | 5.5  | 1.2  | 3   | 7   |
| Prosocial behavior     | 5.8  | 1.5  | 3   | 7   |
| Life purpose           | 6.2  | 1.8  | 4   | 8   |
| Meaning in life        | 6.5  | 1.5  | 4   | 8   |
| Existential well-being | 6.8  | 1.2  | 4   | 8   |
| Overall well-being     | 7.2  | 1.5  | 5   | 9   |

| Variable                     | Mean | SD   | Min | Max |
|------------------------------|------|------|-----|-----|
| Age                          | 34.5 | 10.2 | 18  | 65  |
| Gender                       | 1.2  | 0.4  | 0   | 2   |
| Marital status               | 1.5  | 0.5  | 0   | 3   |
| Education                    | 12.5 | 1.5  | 9   | 16  |
| Income                       | 15.2 | 3.8  | 10  | 25  |
| Occupation                   | 1.8  | 0.8  | 0   | 4   |
| Health status                | 1.1  | 0.3  | 0   | 2   |
| Stress level                 | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction            | 3.2  | 1.5  | 1   | 5   |
| Resilience                   | 2.8  | 1.1  | 1   | 5   |
| Optimism                     | 3.5  | 1.3  | 1   | 5   |
| Gratitude                    | 3.8  | 1.4  | 1   | 5   |
| Forgiveness                  | 3.1  | 1.2  | 1   | 5   |
| Empathy                      | 3.4  | 1.3  | 1   | 5   |
| Compassion                   | 3.6  | 1.4  | 1   | 5   |
| Kindness                     | 3.3  | 1.2  | 1   | 5   |
| Generosity                   | 3.7  | 1.5  | 1   | 5   |
| Patience                     | 3.9  | 1.6  | 1   | 5   |
| Humility                     | 3.2  | 1.3  | 1   | 5   |
| Modesty                      | 3.5  | 1.4  | 1   | 5   |
| Shyness                      | 2.9  | 1.1  | 1   | 5   |
| Introversion                 | 2.7  | 1.0  | 1   | 5   |
| Extroversion                 | 2.8  | 1.1  | 1   | 5   |
| Sensitivity                  | 3.0  | 1.2  | 1   | 5   |
| Emotionality                 | 3.1  | 1.3  | 1   | 5   |
| Imagination                  | 3.3  | 1.4  | 1   | 5   |
| Creativity                   | 3.4  | 1.5  | 1   | 5   |
| Curiosity                    | 3.6  | 1.6  | 1   | 5   |
| Openness                     | 3.7  | 1.7  | 1   | 5   |
| Conscientiousness            | 3.8  | 1.8  | 1   | 5   |
| Agreeableness                | 3.9  | 1.9  | 1   | 5   |
| Neuroticism                  | 2.5  | 1.0  | 1   | 5   |
| Stability                    | 2.4  | 0.9  | 1   | 5   |
| Control                      | 2.6  | 1.1  | 1   | 5   |
| Order                        | 2.7  | 1.2  | 1   | 5   |
| Discipline                   | 2.8  | 1.3  | 1   | 5   |
| Responsibility               | 2.9  | 1.4  | 1   | 5   |
| Reliability                  | 3.0  | 1.5  | 1   | 5   |
| Trustworthiness              | 3.1  | 1.6  | 1   | 5   |
| Honesty                      | 3.2  | 1.7  | 1   | 5   |
| Integrity                    | 3.3  | 1.8  | 1   | 5   |
| Authenticity                 | 3.4  | 1.9  | 1   | 5   |
| Genuineness                  | 3.5  | 2.0  | 1   | 5   |
| Transparency                 | 3.6  | 2.1  | 1   | 5   |
| Openness to experience       | 3.7  | 2.2  | 1   | 5   |
| Conscientiousness to action  | 3.8  | 2.3  | 1   | 5   |
| Agreeableness to others      | 3.9  | 2.4  | 1   | 5   |
| Neuroticism to self          | 2.5  | 1.0  | 1   | 5   |
| Stability to mind            | 2.4  | 0.9  | 1   | 5   |
| Control to behavior          | 2.6  | 1.1  | 1   | 5   |
| Order to life                | 2.7  | 1.2  | 1   | 5   |
| Discipline to work           | 2.8  | 1.3  | 1   | 5   |
| Responsibility to family     | 2.9  | 1.4  | 1   | 5   |
| Reliability to friends       | 3.0  | 1.5  | 1   | 5   |
| Trustworthiness to society   | 3.1  | 1.6  | 1   | 5   |
| Honesty to self              | 3.2  | 1.7  | 1   | 5   |
| Integrity to others          | 3.3  | 1.8  | 1   | 5   |
| Authenticity to world        | 3.4  | 1.9  | 1   | 5   |
| Genuineness to nature        | 3.5  | 2.0  | 1   | 5   |
| Transparency to universe     | 3.6  | 2.1  | 1   | 5   |
| Openness to cosmos           | 3.7  | 2.2  | 1   | 5   |
| Conscientiousness to destiny | 3.8  | 2.3  | 1   | 5   |
| Agreeableness to fate        | 3.9  | 2.4  | 1   | 5   |
| Neuroticism to chance        | 2.5  | 1.0  | 1   | 5   |
| Stability to luck            | 2.4  | 0.9  | 1   | 5   |
| Control to karma             | 2.6  | 1.1  | 1   | 5   |
| Order to destiny             | 2.7  | 1.2  | 1   | 5   |
| Discipline to fate           | 2.8  | 1.3  | 1   | 5   |
| Responsibility to chance     | 2.9  | 1.4  | 1   | 5   |
| Reliability to luck          | 3.0  | 1.5  | 1   | 5   |
| Trustworthiness to karma     | 3.1  | 1.6  | 1   | 5   |
| Honesty to destiny           | 3.2  | 1.7  | 1   | 5   |
| Integrity to fate            | 3.3  | 1.8  | 1   | 5   |
| Authenticity to chance       | 3.4  | 1.9  | 1   | 5   |
| Genuineness to luck          | 3.5  | 2.0  | 1   | 5   |
| Transparency to karma        | 3.6  | 2.1  | 1   | 5   |
| Openness to destiny          | 3.7  | 2.2  | 1   | 5   |
| Conscientiousness to fate    | 3.8  | 2.3  | 1   | 5   |
| Agreeableness to chance      | 3.9  | 2.4  | 1   | 5   |

| Variable                        | Mean | SD   | Min | Max |
|---------------------------------|------|------|-----|-----|
| Age                             | 34.5 | 10.2 | 21  | 55  |
| Gender                          | 1.2  | 0.4  | 1   | 2   |
| Marital status                  | 1.5  | 0.5  | 1   | 3   |
| Education                       | 12.5 | 1.5  | 9   | 16  |
| Income                          | 1.8  | 0.8  | 1   | 3   |
| Occupation                      | 1.5  | 0.5  | 1   | 3   |
| Religion                        | 1.2  | 0.4  | 1   | 2   |
| Health status                   | 1.5  | 0.5  | 1   | 3   |
| Stress level                    | 2.5  | 1.0  | 1   | 4   |
| Life satisfaction               | 3.5  | 1.0  | 1   | 5   |
| Work-life balance               | 2.5  | 1.0  | 1   | 4   |
| Family support                  | 3.0  | 1.0  | 1   | 4   |
| Community support               | 2.5  | 1.0  | 1   | 4   |
| Healthcare access               | 3.0  | 1.0  | 1   | 4   |
| Education access                | 3.5  | 1.0  | 1   | 4   |
| Income stability                | 2.5  | 1.0  | 1   | 4   |
| Occupational satisfaction       | 3.0  | 1.0  | 1   | 4   |
| Religious participation         | 2.0  | 1.0  | 1   | 3   |
| Healthcare utilization          | 2.5  | 1.0  | 1   | 4   |
| Education attainment            | 3.0  | 1.0  | 1   | 4   |
| Income growth                   | 2.0  | 1.0  | 1   | 3   |
| Occupational advancement        | 2.5  | 1.0  | 1   | 4   |
| Religious commitment            | 2.0  | 1.0  | 1   | 3   |
| Healthcare coverage             | 3.0  | 1.0  | 1   | 4   |
| Education enrollment            | 3.5  | 1.0  | 1   | 4   |
| Income security                 | 2.5  | 1.0  | 1   | 4   |
| Occupational engagement         | 3.0  | 1.0  | 1   | 4   |
| Religious observance            | 2.0  | 1.0  | 1   | 3   |
| Healthcare quality              | 3.0  | 1.0  | 1   | 4   |
| Education quality               | 3.5  | 1.0  | 1   | 4   |
| Income growth rate              | 2.0  | 1.0  | 1   | 3   |
| Occupational satisfaction index | 2.5  | 1.0  | 1   | 4   |
| Religious participation index   | 2.0  | 1.0  | 1   | 3   |
| Healthcare utilization index    | 2.5  | 1.0  | 1   | 4   |
| Education attainment index      | 3.0  | 1.0  | 1   | 4   |
| Income growth index             | 2.0  | 1.0  | 1   | 3   |
| Occupational advancement index  | 2.5  | 1.0  | 1   | 4   |
| Religious commitment index      | 2.0  | 1.0  | 1   | 3   |
| Healthcare coverage index       | 3.0  | 1.0  | 1   | 4   |
| Education enrollment index      | 3.5  | 1.0  | 1   | 4   |
| Income security index           | 2.5  | 1.0  | 1   | 4   |
| Occupational engagement index   | 3.0  | 1.0  | 1   | 4   |
| Religious observance index      | 2.0  | 1.0  | 1   | 3   |
| Healthcare quality index        | 3.0  | 1.0  | 1   | 4   |
| Education quality index         | 3.5  | 1.0  | 1   | 4   |
| Income growth rate index        | 2.0  | 1.0  | 1   | 3   |
| Occupational satisfaction index | 2.5  | 1.0  | 1   | 4   |
| Religious participation index   | 2.0  | 1.0  | 1   | 3   |
| Healthcare utilization index    | 2.5  | 1.0  | 1   | 4   |
| Education attainment index      | 3.0  | 1.0  | 1   | 4   |
| Income growth index             | 2.0  | 1.0  | 1   | 3   |
| Occupational advancement index  | 2.5  | 1.0  | 1   | 4   |
| Religious commitment index      | 2.0  | 1.0  | 1   | 3   |
| Healthcare coverage index       | 3.0  | 1.0  | 1   | 4   |
| Education enrollment index      | 3.5  | 1.0  | 1   | 4   |
| Income security index           | 2.5  | 1.0  | 1   | 4   |
| Occupational engagement index   | 3.0  | 1.0  | 1   | 4   |
| Religious observance index      | 2.0  | 1.0  | 1   | 3   |
| Healthcare quality index        | 3.0  | 1.0  | 1   | 4   |
| Education quality index         | 3.5  | 1.0  | 1   | 4   |
| Income growth rate index        | 2.0  | 1.0  | 1   | 3   |
| Occupational satisfaction index | 2.5  | 1.0  | 1   | 4   |
| Religious participation index   | 2.0  | 1.0  | 1   | 3   |
| Healthcare utilization index    | 2.5  | 1.0  | 1   | 4   |
| Education attainment index      | 3.0  | 1.0  | 1   | 4   |
| Income growth index             | 2.0  | 1.0  | 1   | 3   |
| Occupational advancement index  | 2.5  | 1.0  | 1   | 4   |
| Religious commitment index      | 2.0  | 1.0  | 1   | 3   |
| Healthcare coverage index       | 3.0  | 1.0  | 1   | 4   |
| Education enrollment index      | 3.5  | 1.0  | 1   | 4   |
| Income security index           | 2.5  | 1.0  | 1   | 4   |
| Occupational engagement index   | 3.0  | 1.0  | 1   | 4   |
| Religious observance index      | 2.0  | 1.0  | 1   | 3   |
| Healthcare quality index        | 3.0  | 1.0  | 1   | 4   |
| Education quality index         | 3.5  | 1.0  | 1   | 4   |
| Income growth rate index        | 2.0  | 1.0  | 1   | 3   |
| Occupational satisfaction index | 2.5  | 1.0  | 1   | 4   |
| Religious participation index   | 2.0  | 1.0  | 1   | 3   |
| Healthcare utilization index    | 2.5  | 1.0  | 1   | 4   |
| Education attainment index      | 3.0  | 1.0  | 1   | 4   |
| Income growth index             | 2.0  | 1.0  | 1   | 3   |
| Occupational advancement index  | 2.5  | 1.0  | 1   | 4   |
| Religious commitment index      | 2.0  | 1.0  | 1   | 3   |
| Healthcare coverage index       | 3.0  | 1.0  |     |     |

| Variable               | Mean | SD   | Min | Max |
|------------------------|------|------|-----|-----|
| Age                    | 34.5 | 10.2 | 21  | 55  |
| Gender                 | 1.2  | 0.4  | 1   | 2   |
| Marital status         | 1.5  | 0.5  | 1   | 3   |
| Education              | 12.5 | 1.5  | 9   | 16  |
| Income                 | 15.2 | 3.8  | 10  | 25  |
| Occupation             | 1.8  | 0.8  | 1   | 4   |
| Health status          | 1.2  | 0.3  | 1   | 2   |
| Stress level           | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction      | 3.8  | 1.5  | 2   | 6   |
| Work-life balance      | 2.2  | 1.0  | 1   | 4   |
| Family support         | 1.5  | 0.7  | 1   | 3   |
| Community involvement  | 1.8  | 0.9  | 1   | 4   |
| Personal growth        | 2.0  | 1.1  | 1   | 4   |
| Financial stability    | 1.5  | 0.8  | 1   | 3   |
| Emotional well-being   | 2.5  | 1.0  | 1   | 4   |
| Physical health        | 1.8  | 0.7  | 1   | 3   |
| Social relationships   | 2.2  | 1.0  | 1   | 4   |
| Work environment       | 1.5  | 0.8  | 1   | 3   |
| Leadership skills      | 2.0  | 1.1  | 1   | 4   |
| Team collaboration     | 2.5  | 1.0  | 1   | 4   |
| Communication skills   | 2.8  | 1.2  | 1   | 5   |
| Problem-solving skills | 3.0  | 1.3  | 1   | 5   |
| Time management        | 2.5  | 1.0  | 1   | 4   |
| Decision-making skills | 2.8  | 1.1  | 1   | 4   |
| Adaptability           | 2.2  | 1.0  | 1   | 4   |
| Resilience             | 2.0  | 1.1  | 1   | 4   |
| Self-awareness         | 2.5  | 1.0  | 1   | 4   |
| Empathy                | 2.8  | 1.2  | 1   | 5   |
| Conflict resolution    | 2.5  | 1.0  | 1   | 4   |
| Networking             | 2.0  | 1.1  | 1   | 4   |
| Continuous learning    | 2.5  | 1.0  | 1   | 4   |
| Goal setting           | 2.8  | 1.2  | 1   | 5   |
| Accountability         | 2.5  | 1.0  | 1   | 4   |
| Positive mindset       | 3.0  | 1.3  | 1   | 5   |
| Gratitude              | 2.8  | 1.2  | 1   | 5   |
| Optimism               | 3.2  | 1.4  | 1   | 5   |
| Perseverance           | 2.5  | 1.0  | 1   | 4   |
| Self-discipline        | 2.8  | 1.1  | 1   | 4   |
| Patience               | 2.5  | 1.0  | 1   | 4   |
| Humility               | 2.2  | 1.0  | 1   | 4   |
| Kindness               | 2.8  | 1.2  | 1   | 5   |
| Generosity             | 2.5  | 1.0  | 1   | 4   |
| Forgiveness            | 2.8  | 1.1  | 1   | 4   |
| Compassion             | 3.0  | 1.3  | 1   | 5   |
| Respect                | 3.2  | 1.4  | 1   | 5   |
| Integrity              | 3.5  | 1.5  | 1   | 5   |
| Honesty                | 3.8  | 1.6  | 1   | 5   |
| Trustworthiness        | 3.5  | 1.5  | 1   | 5   |
| Reliability            | 3.2  | 1.4  | 1   | 5   |
| Consistency            | 3.0  | 1.3  | 1   | 5   |
| Stability              | 2.8  | 1.2  | 1   | 5   |
| Endurance              | 2.5  | 1.0  | 1   | 4   |
| Strength               | 2.2  | 1.0  | 1   | 4   |
| Power                  | 2.0  | 1.1  | 1   | 4   |
| Influence              | 1.8  | 0.9  | 1   | 3   |
| Authority              | 1.5  | 0.8  | 1   | 3   |
| Leadership             | 1.2  | 0.7  | 1   | 3   |
| Management             | 1.0  | 0.6  | 1   | 3   |
| Organization           | 0.8  | 0.5  | 1   | 3   |
| Coordination           | 0.5  | 0.4  | 1   | 3   |
| Collaboration          | 0.3  | 0.3  | 1   | 3   |
| Partnership            | 0.2  | 0.2  | 1   | 3   |
| Teamwork               | 0.1  | 0.1  | 1   | 3   |
| Cooperation            | 0.0  | 0.0  | 1   | 3   |
| Unity                  | 0.0  | 0.0  | 1   | 3   |
| Harmony                | 0.0  | 0.0  | 1   | 3   |
| Balance                | 0.0  | 0.0  | 1   | 3   |
| Equilibrium            | 0.0  | 0.0  | 1   | 3   |
| Steadiness             | 0.0  | 0.0  | 1   | 3   |
| Consistency            | 0.0  | 0.0  | 1   | 3   |
| Reliability            | 0.0  | 0.0  | 1   | 3   |
| Trustworthiness        | 0.0  | 0.0  | 1   | 3   |
| Integrity              | 0.0  | 0.0  | 1   | 3   |
| Honesty                | 0.0  | 0.0  | 1   | 3   |
| Transparency           | 0.0  | 0.0  | 1   | 3   |
| Openness               | 0.0  | 0.0  | 1   | 3   |
| Accessibility          | 0.0  | 0.0  | 1   | 3   |
| Availability           | 0.0  | 0.0  | 1   | 3   |
| Proximity              | 0.0  | 0.0  | 1   | 3   |
| Reachability           | 0.0  | 0.0  | 1   | 3   |
| Connectivity           | 0.0  | 0.0  | 1   | 3   |
| Interconnectedness     | 0.0  | 0.0  | 1   | 3   |
| Network                | 0.0  | 0.0  | 1   | 3   |
| Web                    | 0.0  | 0.0  | 1   | 3   |
| Grid                   | 0.0  | 0.0  | 1   | 3   |
| System                 | 0.0  | 0.0  |     |     |

| Variable                      | Mean | SD   | Min | Max |
|-------------------------------|------|------|-----|-----|
| Age                           | 34.5 | 10.2 | 21  | 55  |
| Gender                        | 1.2  | 0.4  | 1   | 2   |
| Marital status                | 1.5  | 0.5  | 1   | 3   |
| Education                     | 12.5 | 1.5  | 9   | 16  |
| Income                        | 1.8  | 0.8  | 1   | 3   |
| Occupation                    | 1.5  | 0.5  | 1   | 3   |
| Health status                 | 1.2  | 0.4  | 1   | 2   |
| Stress level                  | 2.5  | 1.2  | 1   | 4   |
| Life satisfaction             | 3.5  | 1.5  | 1   | 5   |
| Resilience                    | 2.8  | 1.0  | 1   | 4   |
| Optimism                      | 3.2  | 1.2  | 1   | 4   |
| Self-efficacy                 | 3.0  | 1.0  | 1   | 4   |
| Emotional stability           | 2.5  | 0.8  | 1   | 3   |
| Neuroticism                   | 1.5  | 0.5  | 1   | 2   |
| Extraversion                  | 2.8  | 0.8  | 1   | 3   |
| Conscientiousness             | 3.0  | 0.8  | 1   | 3   |
| Agreeableness                 | 2.5  | 0.8  | 1   | 3   |
| Openness                      | 2.2  | 0.8  | 1   | 3   |
| Depression                    | 1.2  | 0.4  | 1   | 2   |
| Anxiety                       | 1.5  | 0.5  | 1   | 2   |
| Substance use                 | 0.5  | 0.5  | 0   | 1   |
| Alcohol consumption           | 1.0  | 0.5  | 0   | 2   |
| Drug use                      | 0.2  | 0.2  | 0   | 1   |
| Smoking                       | 0.8  | 0.8  | 0   | 1   |
| Exercise frequency            | 2.0  | 1.0  | 0   | 3   |
| Diet quality                  | 2.5  | 1.0  | 1   | 3   |
| Sleep quality                 | 2.0  | 0.8  | 1   | 3   |
| Work-life balance             | 2.2  | 0.8  | 1   | 3   |
| Family support                | 2.5  | 0.8  | 1   | 3   |
| Community support             | 2.0  | 0.8  | 1   | 3   |
| Religious/spiritual beliefs   | 2.5  | 0.8  | 1   | 3   |
| Philosophical beliefs         | 2.2  | 0.8  | 1   | 3   |
| Environmental beliefs         | 2.0  | 0.8  | 1   | 3   |
| Political beliefs             | 2.5  | 0.8  | 1   | 3   |
| Ethical beliefs               | 2.2  | 0.8  | 1   | 3   |
| Artistic beliefs              | 2.0  | 0.8  | 1   | 3   |
| Scientific beliefs            | 2.5  | 0.8  | 1   | 3   |
| Religious/spiritual practices | 2.0  | 0.8  | 1   | 3   |
| Philosophical practices       | 1.8  | 0.8  | 1   | 3   |
| Environmental practices       | 1.5  | 0.8  | 1   | 3   |
| Political practices           | 2.0  | 0.8  | 1   | 3   |
| Ethical practices             | 1.8  | 0.8  | 1   | 3   |
| Artistic practices            | 1.5  | 0.8  | 1   | 3   |
| Scientific practices          | 2.0  | 0.8  | 1   | 3   |

| Variable                  | Mean | SD   | Min | Max |
|---------------------------|------|------|-----|-----|
| Age                       | 35.2 | 12.5 | 18  | 65  |
| Gender                    | 1.2  | 0.4  | 1   | 2   |
| Marital status            | 1.5  | 0.5  | 1   | 3   |
| Education                 | 12.8 | 2.1  | 9   | 16  |
| Income                    | 15.5 | 3.2  | 10  | 25  |
| Occupation                | 1.8  | 0.6  | 1   | 3   |
| Health status             | 1.2  | 0.3  | 1   | 2   |
| Stress level              | 2.5  | 1.0  | 1   | 4   |
| Life satisfaction         | 3.8  | 0.8  | 3   | 5   |
| Resilience                | 4.2  | 0.5  | 3   | 5   |
| Optimism                  | 4.5  | 0.4  | 3   | 5   |
| Gratitude                 | 4.8  | 0.3  | 3   | 5   |
| Forgiveness               | 4.6  | 0.4  | 3   | 5   |
| Empathy                   | 4.4  | 0.5  | 3   | 5   |
| Compassion                | 4.3  | 0.4  | 3   | 5   |
| Kindness                  | 4.1  | 0.5  | 3   | 5   |
| Generosity                | 4.0  | 0.4  | 3   | 5   |
| Patience                  | 3.9  | 0.5  | 3   | 5   |
| Self-control              | 3.7  | 0.4  | 3   | 5   |
| Emotional stability       | 3.6  | 0.5  | 3   | 5   |
| Psychological well-being  | 3.5  | 0.4  | 3   | 5   |
| Life purpose              | 3.4  | 0.5  | 3   | 5   |
| Meaning in life           | 3.3  | 0.4  | 3   | 5   |
| Existential well-being    | 3.2  | 0.5  | 3   | 5   |
| Transcendental well-being | 3.1  | 0.4  | 3   | 5   |
| Overall well-being        | 3.0  | 0.5  | 3   | 5   |

| Variable               | Mean | SD   | Min | Max |
|------------------------|------|------|-----|-----|
| Age                    | 34.5 | 12.5 | 18  | 65  |
| Gender                 | 1.2  | 0.4  | 1   | 2   |
| Marital status         | 1.5  | 0.5  | 1   | 3   |
| Education              | 12.5 | 2.5  | 9   | 16  |
| Income                 | 15.5 | 3.5  | 10  | 25  |
| Occupation             | 1.5  | 0.5  | 1   | 3   |
| Religion               | 1.5  | 0.5  | 1   | 3   |
| Health status          | 1.5  | 0.5  | 1   | 3   |
| Stress level           | 1.5  | 0.5  | 1   | 3   |
| Life satisfaction      | 1.5  | 0.5  | 1   | 3   |
| Work-life balance      | 1.5  | 0.5  | 1   | 3   |
| Family support         | 1.5  | 0.5  | 1   | 3   |
| Community support      | 1.5  | 0.5  | 1   | 3   |
| Healthcare access      | 1.5  | 0.5  | 1   | 3   |
| Financial stability    | 1.5  | 0.5  | 1   | 3   |
| Education quality      | 1.5  | 0.5  | 1   | 3   |
| Healthcare quality     | 1.5  | 0.5  | 1   | 3   |
| Work environment       | 1.5  | 0.5  | 1   | 3   |
| Family environment     | 1.5  | 0.5  | 1   | 3   |
| Community environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Financial environment  | 1.5  | 0.5  | 1   | 3   |
| Education environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Work environment       | 1.5  | 0.5  | 1   | 3   |
| Family environment     | 1.5  | 0.5  | 1   | 3   |
| Community environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Financial environment  | 1.5  | 0.5  | 1   | 3   |
| Education environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Work environment       | 1.5  | 0.5  | 1   | 3   |
| Family environment     | 1.5  | 0.5  | 1   | 3   |
| Community environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Financial environment  | 1.5  | 0.5  | 1   | 3   |
| Education environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Work environment       | 1.5  | 0.5  | 1   | 3   |
| Family environment     | 1.5  | 0.5  | 1   | 3   |
| Community environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Financial environment  | 1.5  | 0.5  | 1   | 3   |
| Education environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Work environment       | 1.5  | 0.5  | 1   | 3   |
| Family environment     | 1.5  | 0.5  | 1   | 3   |
| Community environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Financial environment  | 1.5  | 0.5  | 1   | 3   |
| Education environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Work environment       | 1.5  | 0.5  | 1   | 3   |
| Family environment     | 1.5  | 0.5  | 1   | 3   |
| Community environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Financial environment  | 1.5  | 0.5  | 1   | 3   |
| Education environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Work environment       | 1.5  | 0.5  | 1   | 3   |
| Family environment     | 1.5  | 0.5  | 1   | 3   |
| Community environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Financial environment  | 1.5  | 0.5  | 1   | 3   |
| Education environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Work environment       | 1.5  | 0.5  | 1   | 3   |
| Family environment     | 1.5  | 0.5  | 1   | 3   |
| Community environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Financial environment  | 1.5  | 0.5  | 1   | 3   |
| Education environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Work environment       | 1.5  | 0.5  | 1   | 3   |
| Family environment     | 1.5  | 0.5  | 1   | 3   |
| Community environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Financial environment  | 1.5  | 0.5  | 1   | 3   |
| Education environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Work environment       | 1.5  | 0.5  | 1   | 3   |
| Family environment     | 1.5  | 0.5  | 1   | 3   |
| Community environment  | 1.5  | 0.5  | 1   | 3   |
| Healthcare environment | 1.5  | 0.5  | 1   | 3   |
| Financial environment  | 1.5  | 0.5  | 1   | 3   |
| Education environment  | 1    |      |     |     |

| Variable          | Mean | SD   | Min | Max |
|-------------------|------|------|-----|-----|
| Age               | 34.5 | 10.2 | 18  | 65  |
| Gender            | 1.2  | 0.4  | 0   | 2   |
| Marital status    | 1.5  | 0.5  | 0   | 3   |
| Education         | 12.5 | 1.5  | 9   | 16  |
| Income            | 15.2 | 3.8  | 10  | 25  |
| Occupation        | 1.8  | 0.8  | 0   | 4   |
| Health status     | 1.2  | 0.4  | 0   | 2   |
| Stress level      | 2.5  | 1.2  | 1   | 5   |
| Life satisfaction | 3.8  | 1.5  | 2   | 6   |
| Resilience        | 4.2  | 1.8  | 2   | 7   |
| Optimism          | 4.5  | 1.5  | 2   | 7   |
| Gratitude         | 4.8  | 1.2  | 3   | 7   |
| Forgiveness       | 5.2  | 1.5  | 3   | 7   |
| Empathy           | 5.5  | 1.2  | 3   | 7   |
| Compassion        | 5.8  | 1.5  | 3   | 7   |
| Kindness          | 6.2  | 1.2  | 4   | 7   |
| Generosity        | 6.5  | 1.5  | 4   | 7   |
| Patience          | 6.8  | 1.2  | 4   | 7   |
| Humility          | 7.2  | 1.5  | 5   | 7   |
| Modesty           | 7.5  | 1.2  | 5   | 7   |
| Self-control      | 7.8  | 1.5  | 5   | 7   |
| Discipline        | 8.2  | 1.2  | 6   | 7   |
| Perseverance      | 8.5  | 1.5  | 6   | 7   |
| Determination     | 8.8  | 1.2  | 6   | 7   |
| Resolve           | 9.2  | 1.5  | 7   | 7   |
| Willpower         | 9.5  | 1.2  | 7   | 7   |
| Strength          | 9.8  | 1.5  | 7   | 7   |
| Courage           | 10.2 | 1.2  | 7   | 7   |
| Bravery           | 10.5 | 1.5  | 7   | 7   |
| Valor             | 10.8 | 1.2  | 7   | 7   |
| Heroism           | 11.2 | 1.5  | 7   | 7   |
| Integrity         | 11.5 | 1.2  | 7   | 7   |
| Honesty           | 11.8 | 1.5  | 7   | 7   |
| Truthfulness      | 12.2 | 1.2  | 7   | 7   |
| Openness          | 12.5 | 1.5  | 7   | 7   |
| Transparency      | 12.8 | 1.2  | 7   | 7   |
| Authenticity      | 13.2 | 1.5  | 7   | 7   |
| Genuineness       | 13.5 | 1.2  | 7   | 7   |
| Sincerity         | 13.8 | 1.5  | 7   | 7   |
| Frankness         | 14.2 | 1.2  | 7   | 7   |
| Directness        | 14.5 | 1.5  | 7   | 7   |
| Clarity           | 14.8 | 1.2  | 7   | 7   |
| 明瞭                | 15.2 | 1.5  | 7   | 7   |
| 明澈                | 15.5 | 1.2  | 7   | 7   |
| 明淨                | 15.8 | 1.5  | 7   | 7   |
| 明達                | 16.2 | 1.2  | 7   | 7   |
| 明慧                | 16.5 | 1.5  | 7   | 7   |
| 明智                | 16.8 | 1.2  | 7   | 7   |
| 明辨                | 17.2 | 1.5  | 7   | 7   |
| 明察                | 17.5 | 1.2  | 7   | 7   |
| 明瞭                | 17.8 | 1.5  | 7   | 7   |
| 明達                | 18.2 | 1.2  | 7   | 7   |
| 明慧                | 18.5 | 1.5  | 7   | 7   |
| 明智                | 18.8 | 1.2  | 7   | 7   |
| 明辨                | 19.2 | 1.5  | 7   | 7   |
| 明察                | 19.5 | 1.2  | 7   | 7   |
| 明瞭                | 19.8 | 1.5  | 7   | 7   |
| 明達                | 20.2 | 1.2  | 7   | 7   |
| 明慧                | 20.5 | 1.5  | 7   | 7   |
| 明智                | 20.8 | 1.2  | 7   | 7   |
| 明辨                | 21.2 | 1.5  | 7   | 7   |
| 明察                | 21.5 | 1.2  | 7   | 7   |
| 明瞭                | 21.8 | 1.5  | 7   | 7   |
| 明達                | 22.2 | 1.2  | 7   | 7   |
| 明慧                | 22.5 | 1.5  | 7   | 7   |
| 明智                | 22.8 | 1.2  | 7   | 7   |
| 明辨                | 23.2 | 1.5  | 7   | 7   |
| 明察                | 23.5 | 1.2  | 7   | 7   |
| 明瞭                | 23.8 | 1.5  | 7   | 7   |
| 明達                | 24.2 | 1.2  | 7   | 7   |
| 明慧                | 24.5 | 1.5  | 7   | 7   |
| 明智                | 24.8 | 1.2  | 7   | 7   |
| 明辨                | 25.2 | 1.5  | 7   | 7   |
| 明察                | 25.5 | 1.2  | 7   | 7   |
| 明瞭                | 25.8 | 1.5  | 7   | 7   |
| 明達                | 26.2 | 1.2  | 7   | 7   |
| 明慧                | 26.5 | 1.5  | 7   | 7   |
| 明智                | 26.8 | 1.2  | 7   | 7   |
| 明辨                | 27.2 | 1.5  | 7   | 7   |
| 明察                | 27.5 | 1.2  | 7   | 7   |
| 明瞭                | 27.8 | 1.5  | 7   | 7   |
| 明達                | 28.2 | 1.2  | 7   | 7   |
| 明慧                | 28.5 | 1.5  | 7   | 7   |
| 明智                | 28.8 | 1.2  | 7   | 7   |
| 明辨                | 29.2 | 1.5  |     |     |

| Variable              | Mean | SD   | Min | Max |
|-----------------------|------|------|-----|-----|
| Age                   | 34.5 | 12.5 | 18  | 65  |
| Gender                | 1.2  | 0.4  | 1   | 2   |
| Marital status        | 1.5  | 0.5  | 1   | 3   |
| Education             | 12.5 | 2.5  | 9   | 16  |
| Income                | 15.5 | 3.5  | 10  | 25  |
| Occupation            | 1.5  | 0.5  | 1   | 3   |
| Religion              | 1.5  | 0.5  | 1   | 3   |
| Health status         | 1.5  | 0.5  | 1   | 3   |
| Stress level          | 1.5  | 0.5  | 1   | 3   |
| Life satisfaction     | 1.5  | 0.5  | 1   | 3   |
| Work-life balance     | 1.5  | 0.5  | 1   | 3   |
| Family support        | 1.5  | 0.5  | 1   | 3   |
| Community support     | 1.5  | 0.5  | 1   | 3   |
| Healthcare access     | 1.5  | 0.5  | 1   | 3   |
| Financial stability   | 1.5  | 0.5  | 1   | 3   |
| Education level       | 12.5 | 2.5  | 9   | 16  |
| Income level          | 15.5 | 3.5  | 10  | 25  |
| Occupational status   | 1.5  | 0.5  | 1   | 3   |
| Religious affiliation | 1.5  | 0.5  | 1   | 3   |
| Health status         | 1.5  | 0.5  | 1   | 3   |
| Stress level          | 1.5  | 0.5  | 1   | 3   |
| Life satisfaction     | 1.5  | 0.5  | 1   | 3   |
| Work-life balance     | 1.5  | 0.5  | 1   | 3   |
| Family support        | 1.5  | 0.5  | 1   | 3   |
| Community support     | 1.5  | 0.5  | 1   | 3   |
| Healthcare access     | 1.5  | 0.5  | 1   | 3   |
| Financial stability   | 1.5  | 0.5  | 1   | 3   |

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CG43980889





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<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1096

Asp Leu Leu Lys Glu Lys Val Ser Ile Tyr Gln Asn Gln Asn

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<210> 1097

<211> 14

<212> PRT

<213> Homo sapiens

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<400> 1097

Glu Ile Pro Ser Lys Glu Arg Pro Tyr Asp Ala Ala Lys Asp

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<210> 1102  
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<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1102  
Arg Gly Leu Ala Ser Ala Val Lys Gly Gly His Gly Gly Ala  
1 5 10

<210> 1103  
<211> 14  
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<213> Homo sapiens

<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1103  
Lys Lys Asp Asp Val Thr Ala Gly Lys Lys Pro Phe Arg Pro  
1 5 10

<210> 1104  
<211> 14  
<212> PRT  
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<400> 1104  
Asn Phe Phe Lys Leu Asn Asp Lys Ser Glu Lys Asp Lys Lys  
1 5 10

<210> 1105  
<211> 14  
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<220>  
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<400> 1105  
His Lys Glu Asp Ala Gly Ala Val Cys Ser Glu His Gln Ser  
1 5 10

<210> 1106

<211> 14  
<212> PRT  
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<223> cSNP translation

<400> 1106  
Leu Lys Lys Ala Arg Thr Gly Leu Gln Met Asp Glu Leu Lys  
1 5 10

<210> 1107  
<211> 14  
<212> PRT  
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<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1107  
Lys Leu Asn Leu Lys Met Lys Glu Glu Tyr Asp Lys Ile Gln  
1 5 10

<210> 1108  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1108  
Leu Met Ser Val Lys Met Ala Lys Lys Tyr Lys Asn Ile Val  
1 5 10

<210> 1109  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1109  
Cys Asp Pro Glu Val Asn Asn Phe Arg Ala Lys Met Cys Gln  
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<210> 1110  
<211> 14

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<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1114

Asn Leu His Thr Leu Asn Asn Tyr Gln Lys Leu Leu Gly Asn  
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<210> 1115

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<400> 1115

Leu Lys Glu Met Lys Glu Val Leu Gly Thr Pro Gly Ala Ala  
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<210> 1116

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1116

Pro Gly Gly Cys Ser Ala Ile Ser Ala His Gly Cys Leu Phe  
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<210> 1117

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 1117

Gly Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Leu  
1 5 10

<210> 1118

<211> 14

<212> PRT

<213> Homo sapiens

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<220>  
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<400> 1118  
Pro Ile Gly Gly Arg Asn Ile Gln Gly Gly Ile Arg Phe Gly  
1 5 10

<210> 1119  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
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<223> cSNP translation

<400> 1119  
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<210> 1120  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
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<223> cSNP translation

<400> 1120  
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1 5 10

<210> 1121  
<211> 14  
<212> PRT  
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<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1121  
Lys Tyr Asp Met Glu Val Lys Val Gln Lys Thr Ser Lys Glu  
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<210> 1122  
<211> 14  
<212> PRT  
<213> Homo sapiens

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<220>  
<221> VARIANT  
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<400> 1122  
Ser Arg Gly Phe Thr Tyr Arg Leu His Phe Trp Leu Gly Lys  
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<210> 1123  
<211> 14  
<212> PRT  
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<220>  
<221> VARIANT  
<222> (7)...(0)  
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<400> 1123  
Met Asn Gln Leu Ser His Ile Asn Leu Ile Gln Leu Tyr Asp  
1 5 10

<210> 1124  
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<212> PRT  
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<220>  
<221> VARIANT  
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<400> 1124  
Leu Thr Glu Leu Asp Val Ile Leu Phe Thr Arg Gln Ile Cys  
1 5 10

<210> 1125  
<211> 14  
<212> PRT  
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<220>  
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<223> cSNP translation

<400> 1125  
Glu Tyr Ala Lys Tyr Cys Thr Glu Ile Leu Gly Val Ala Ala  
1 5 10

<210> 1126  
<211> 14  
<212> PRT  
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<220>

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<221> VARIANT  
<222> (7)...(0)  
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<400> 1126  
Asn Val Gly Pro Gln Met Val Ile Ser Thr Pro Gln Arg Leu  
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<210> 1127  
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<400> 1127  
Ala Ala His Met Ala Ala Ser Ala Ile Leu Asn Leu Ser Thr  
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<210> 1128  
<211> 14  
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<213> Homo sapiens

<220>  
<221> VARIANT  
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<223> cSNP translation

<400> 1128  
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<210> 1129  
<211> 14  
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<220>  
<221> VARIANT  
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<223> cSNP translation

<400> 1129  
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<210> 1130  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT



<223> cSNP translation

<400> 1134

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<210> 1135

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

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Gly Lys Asn Ser Ser Tyr Ala His Gly Gly Leu Asp Ser Asn  
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<210> 1136

<211> 14

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<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 1136

Ser Asn Glu Ser Leu Val Ala Asn Arg Val Thr Gly Asn Phe  
1 5 10

<210> 1137

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1137

Ser Tyr Ser Gln Ala Gly Val Thr Glu Thr Glu Trp Thr Ser  
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<210> 1138

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<400> 1142  
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1 5 10

<210> 1143  
<211> 14  
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<221> VARIANT  
<222> (7)...(0)  
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<400> 1143  
Tyr Ser Ser Ser Gly Pro Asp Leu Arg Arg Ser Leu Phe Ser  
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<210> 1144  
<211> 14  
<212> PRT  
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<220>  
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<223> cSNP translation

<400> 1144  
Gln Pro Ala Pro Ser Pro Asp Asp Leu Ala Leu Ser Met Gly  
1 5 10

<210> 1145  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1145  
Phe Asp Phe Gln Val Gly Glu Glu Ala Pro Ile Leu Pro Asp  
1 5 10

<210> 1146  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1146

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Leu Gln Glu Lys Leu Trp Val Ile Leu Gln Ala Thr Tyr Ile  
1 5 10

<210> 1147  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1147  
Cys Gly Lys Ser Val Tyr Val Ala Glu Lys Val Met Gly Gly  
1 5 10

<210> 1148  
<211> 14  
<212> PRT  
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<220>  
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<400> 1148  
Lys Ser Lys Ser Asn Ser Thr Ala Ala Arg Glu Pro Asn Gly  
1 5 10

<210> 1149  
<211> 14  
<212> PRT  
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<220>  
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<400> 1149  
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<210> 1150  
<211> 14  
<212> PRT  
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<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1150  
Gln Leu Gln Leu Gln Ala Val His Ala Gln Glu Gln Ile Cys

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1 5 10

<210> 1151  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7) ..(0)  
<223> cSNP translation

<400> 1151  
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1 5 10

<210> 1152  
<211> 14  
<212> PRT  
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<220>  
<221> VARIANT  
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<223> cSNP translation

<400> 1152  
Gly Lys Arg Leu Phe Val Ile Lys Pro Ser Leu Tyr Tyr Asp  
1 5 10

<210> 1153  
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<212> PRT  
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<220>  
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<222> (7)...(0)  
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<400> 1153  
Leu Val Pro Asp Glu Asp Val Arg Ala Ala Lys Trp Ala Val  
1 5 10

<210> 1154  
<211> 14  
<212> PRT  
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<220>  
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<222> (7)...(0)  
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<400> 1154  
Val Val Arg Asn Ser Pro Arg Gly Val Lys Val Gln Met Ala  
1 5 10

<210> 1155  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
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<400> 1155  
Ala Leu Ser Ala Trp Pro Gln Leu Asp Gln Ala Ser Arg Cys  
1 5 10

<210> 1156  
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<400> 1156  
Ile Trp Ser Phe Cys Phe Tyr Val Val Thr Val Phe Ser Val  
1 5 10

<210> 1157  
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<220>  
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Asn Leu Ser Asn Phe Leu Asn Lys Ser Gly Leu Gln Gly Tyr  
1 5 10

<210> 1158  
<211> 14  
<212> PRT  
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<400> 1158  
Thr Ser Ser Ser Lys Asn Arg Asp Pro Ile Thr Ile Val Asp  
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<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> (7)...(0)  
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<400> 1163  
Gln Pro Ser Thr Ser Thr Asn Gln Pro Val Thr Ser Glu Pro  
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<210> 1164  
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<212> PRT  
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<400> 1164  
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1 5 10

<210> 1165  
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<400> 1165  
Gln Ala Arg His Arg Thr Gly Gly Thr Asn Thr Pro Pro Ser  
1 5 10

<210> 1166  
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<400> 1166  
Phe Lys Asn Ile Lys Ser Ala Thr Glu Leu Asn Gly Asp Ile  
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<210> 1167  
<211> 14

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<212> PRT  
<213> Homo sapiens

<220>  
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<400> 1167  
Glu Leu Ala Ile Asn Pro Val Gly Asp Arg Ile Ile Asn Ala  
1 5 10

<210> 1168  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1168  
Asn Gly Thr Leu Ser Arg Asp Asp Phe Gln Arg Ile Pro Glu  
1 5 10

<210> 1169  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
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<400> 1169  
Lys His Met Glu Met Glu Asp Ile Ser Ser Glu Glu Val Val  
1 5 10

<210> 1170  
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<212> PRT  
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<220>  
<221> VARIANT  
<222> (7)...(0)  
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<400> 1170  
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1 5 10

<210> 1171  
<211> 14  
<212> PRT

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&lt;221&gt; VARIANT

<223> cSNP translation

Cys Pro Pro Asp Tyr His Tyr Ile His Thr Glu Ile Ser Arg  
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<211> 6

<213> Homo sapiens

<221> VARIANT

<223> cSNP translation

Arg His Thr Asp Leu Asp  
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<211> 5

<213> Homo sapiens

Ser Phe Leu Val Arg  
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<211> 14

<213> Homo sapiens

<221> VARIANT

<223> cSNP translation

Gly Ile Pro Gly Gly Pro Gly Gly Pro Gly Cys Gln Glu Leu  
1 5 10

<211> 14

<213> Homo sapiens

<221> VARIANT

<223> cSNP translation

<400> 1175

Lys Tyr His Gly Val Ser Pro Leu Asn Pro Pro Glu Thr Leu  
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<210> 1176

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

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<210> 1177

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

<223> cSNP translation

<400> 1177

Thr Val Tyr Pro Pro Leu Leu Ser Ile Gln Ala His Ser Gly  
1 5 10

<210> 1178

<211> 14

<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> (7)...(0)

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<400> 1178

Leu Ala Leu Pro Ser Val Thr Leu Cys Thr Phe Asn Ser Tyr  
1 5 10

<210> 1179

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 1179  
Pro Asn Val Tyr His Glu Pro Lys Leu Ala Ala Lys Glu Tyr  
1 5 10

<210> 1180  
<211> 14  
<212> PRT  
<213> Hcmo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1180  
Asn Leu Gln Ser Lys Thr Ala Gly Leu His Val Thr Glu Tyr  
1 5 10

<210> 1181  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1181  
Ser Ser Ile Ile Ala Asp Gln Ile Ala Leu Lys Leu Val Gly  
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<210> 1182  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1182  
Ala Gly Gly Ile Arg His Thr Pro Asp Glu Ile Phe Leu Leu  
1 5 10

<210> 1183  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1183

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<210> 1188  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1188  
Glu Asp Phe Lys Lys Asp Val Lys Asn Ser Leu Arg Glu Thr  
1 5 10

<210> 1189  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1189  
Met Lys Asn Ser Leu Arg Gly Thr Gln Glu Asn Ile Asn Lys  
1 5 10

<210> 1190  
<211> 14  
<212> PRT  
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<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1190  
Glu Thr Gln Glu Asn Ile Ser Lys Gln Val Glu Ala Tyr Arg  
1 5 10

<210> 1191  
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<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1191  
Thr Gln Glu Asn Ile Asn Glu Gln Val Glu Ala Tyr Arg Glu  
1 5 10



<210> 1192  
<211> 6  
<212> PRT  
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<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1192  
Ile Val Thr Ala Thr Glu  
1 5

<210> 1193  
<211> 14  
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<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1193  
Met Gly Gly Gly Arg Asp Pro Glu Glu Met Glu Ile Asp Gly  
1 5 10

<210> 1194  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1194  
Glu Val Lys Arg Lys Gln Cys Asp Ala Tyr Gly Ser Ala Gly  
1 5 10

<210> 1195  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1195  
Asn Tyr Arg Asn Asn Pro Ser His Asn Phe Arg His Cys Phe  
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<210> 1196  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1196  
Leu Leu Arg His His Gly Gly Thr Val Leu Pro Ser Leu Asp  
1 5 10

<210> 1197  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1197  
Leu Ser Thr Tyr Ser Leu Asp Trp Val Met Ala Ala Val Val  
1 5 10

<210> 1198  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1198  
Ile Ile Cys Cys Ser Glu Leu Pro Val Val Lys Thr Glu Met  
1 5 10

<210> 1199  
<211> 14  
<212> PRT  
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<220>  
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<400> 1202  
Leu Leu Pro Phe Lys Ser Pro Ser Gly Asn Asp Val Glu Ala  
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<213> Homo sapiens

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<400> 1208

Asp Leu Ile Trp Thr Leu Leu Gln Asp Cys Arg Glu Ile Phe  
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<223> cSNP translation

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Ala Trp Leu Pro Pro Thr Pro Ala Glu His Asp His Ser Leu  
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<223> cSNP translation

<400> 1210

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<210> 1211

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<400> 1211

Gly Asn Ser Arg Val Trp Arg Gly Thr Met Glu Lys Ala Gly  
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<221> VARIANT  
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<223> cSNP translation

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Glu Tyr Gln Val Leu Phe Gly Ala Leu Ile Ser Pro Asp Arg  
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<400> 1230

Gln Arg Asp Leu Gly Tyr Val Pro Leu Val Ser Trp Glu Glu  
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<222> (7)...(0)

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Cys Thr Ala Ser Ala Thr Leu Ser Cys Asn Asp Leu Cys Glu  
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<210> 1234  
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<400> 1235  
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007163314360



Thr Gly Asp Lys Arg Phe Gly Cys Ala Gln Cys Gln Lys Arg  
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<400> 1241  
Thr Ser Val Gly Pro Asn Thr Val Ser Pro Ser Ser Gly Pro  
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<210> 1242  
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<400> 1242  
Cys Glu Gln Gly Phe Ser Arg Lys Ser His Leu Ile Arg His  
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<210> 1243  
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<400> 1243  
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<400> 1244  
Met Ala Leu Phe Thr Pro

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1 5

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<210> 1246  
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1 5 10

<210> 1247  
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<210> 1248  
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<400> 1248  
Thr Pro Gln His Cys Ser Arg Asn Asn Phe Thr Met Arg Leu  
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<210> 1250  
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<210> 1251  
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<400> 1252  
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1 5 10

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<211> 14  
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<220>  
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<400> 1257  
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<210> 1258  
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<400> 1259  
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<210> 1260  
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<400> 1260  
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<210> 1261  
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<400> 1265

Phe Leu Tyr Ile Ser Leu Thr Asp Met Phe Pro Glu Met Asn  
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<210> 1267

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<400> 1268

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<210> 1269

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<210> 1270  
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1 5 10

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<220>  
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Ser His His Asp Pro Ile Ile Lys Val Leu Ser Ile Arg Gly  
1 5 10

<210> 1274  
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<220>  
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<210> 1276  
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<210> 1277  
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<223> cSNP translation

<400> 1285

Ser Ala Ala Ser Ser Val Leu Arg Arg Glu Tyr Lys Pro Arg  
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<210> 1286

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Asp Ile Pro Ile Ile Leu Phe Gly Asn Lys Ser Asp Leu Val  
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<210> 1287

<211> 14

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<222> (7)...(0)

<223> cSNP translation

<400> 1287

Ile Arg Phe Arg Gln Asp Ser Asn Glu Ala Val Gly Gly Phe  
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<210> 1288

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<222> (7)...(0)

<223> cSNP translation

<400> 1288

Thr Thr Val Phe Glu Asp Pro Tyr Asp Tyr Met Asn Ser Leu  
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<210> 1289

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<400> 1293  
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1 5 10

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<400> 1296  
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1 5 10

<210> 1297  
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<223> cSNP translation

<400> 1297



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<210> 1303  
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<400> 1303  
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<400> 1305  
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<223> cSNP translation

<400> 1306  
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<223> cSNP translation

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Gly Gln Glu Tyr His Leu  
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<400> 1308  
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1 5 10

<210> 1309  
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<400> 1309  
Tyr Ser Ser Thr Asp Thr Leu Tyr Pro Gly Ser Leu Pro Pro  
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<210> 1310  
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<400> 1310  
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<223> cSNP translation

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Asn Ser Lys Asp His Leu  
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<210> 1312  
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<210> 1313  
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<400> 1313  
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<210> 1314



<212> PRT  
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<400> 1319  
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<400> 1320  
Ala Leu Thr Ala Leu Ser Gly Arg Arg Ala Gly Thr Arg Leu  
1 5 10

<210> 1321  
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<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1321  
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1 5 10

<210> 1322  
<211> 14  
<212> PRT

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<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1326  
Leu Ser Ala Trp Pro Glu Pro Asp Gln Ala Ser Arg Cys Leu  
1 5 10

<210> 1327  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1327  
Ile Ser Phe Ile Phe Arg Lys Gly Arg Lys Asn Ser Gly Ile  
1 5 10

<210> 1328  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1328  
His Glu Ile Met Gly Pro Glu Lys Lys His Leu Asp Tyr Leu  
1 5 10

<210> 1329  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1329  
Glu Ile Met Gly Pro Lys Asn Lys His Leu Asp Tyr Leu Ile  
1 5 10

<210> 1330  
<211> 14  
<212> PRT  
<213> Homo sapiens

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<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1334  
Met Val Thr Ser Ser Ala Met Ser Ser Leu Ala Cys Ile Ile  
1 5 10

<210> 1335  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1335  
Val Ala Met Leu Leu Pro Asn Trp Lys Thr Ser Ser Tyr Val  
1 5 10

<210> 1336  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
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<400> 1336  
Leu Gln Pro Ser Thr Ser Arg Asp Gln Pro Val Thr Ser Glu  
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<210> 1337  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1337  
Ser Thr Ser Thr Asp Gln Leu Val Thr Ser Glu Pro Thr Ser  
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<210> 1338  
<211> 14  
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<213> Homo sapiens

<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1338  
Thr Asp Gln Pro Val Thr Pro Glu Pro Thr Ser Gln Ala Thr  
1 5 10

<210> 1339  
<211> 14  
<212> PRT  
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<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1339  
Thr Ser Glu Pro Thr Ser Arg Ala Thr Arg Gly Arg Lys Asn  
1 5 10

<210> 1340  
<211> 14  
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<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1340  
Val His Gln Glu Ala Thr Ala Arg Leu Ser Gly Ser Gly Asn  
1 5 10

<210> 1341  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1341  
Arg Ile Lys Met Glu Glu Tyr Ala Leu Leu Ser Asp Pro Val  
1 5 10

<210> 1342  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)

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<223> cSNP translation

<400> 1342

Arg Ala Arg Arg Ser Asn Cys Arg Arg Gln Glu Gly Ile Lys  
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<210> 1343

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)...(0)

<223> cSNP translation

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Gly Trp Arg Ala Ile Asn Ser Ser Met Ala Ala Pro Ser Ser  
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<210> 1344

<211> 14

<212> PRT

<213> Homo sapiens

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<222> (7)...(0)

<223> cSNP translation

<400> 1344

Glu Pro Leu Asn Ser Arg Gly Asn Lys Leu His Phe Ala Phe  
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<210> 1345

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 1345

Ile Asn Pro Leu Gly Asp Trp Ile Ile Asn Ala Phe Phe Pro  
1 5 10

<210> 1346

<211> 14

<212> PRT

<213> Homo sapiens

<220>

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<222> (7)...(0)

<223> cSNP translation

<400> 1346  
Ser Arg Glu Asp Phe Gln Gly Ile Pro Glu Leu Ala Ile Asn  
1 5 10

<210> 1347  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1347  
Leu Glu Gln Glu Tyr Glu Asn Lys Leu Arg Ala Glu Leu Val  
1 5 10

<210> 1348  
<211> 14  
<212> PRT  
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<220>  
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<222> (7)...(0)  
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<400> 1348  
Glu Val Ser Ala Asp Gly Glu Thr Ile Thr Val Thr Phe Phe  
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<210> 1349  
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<212> PRT  
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<220>  
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<400> 1349  
Ala Lys Lys Glu Met Val Ser Ser Lys Leu Pro Asn Ser Val  
1 5 10

<210> 1350  
<211> 14  
<212> PRT  
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<220>  
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Ser Lys Glu Ala Ile His Ile Gln Leu Leu Glu Lys Gln Lys  
1 5 10

<210> 1355  
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<400> 1355  
Val Cys Gly Asp Ala Ser  
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<210> 1356  
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<400> 1356  
Gln Ala Gln Ala Gln Ser Tyr Cys Ser Cys Ser Thr Val Ser  
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<210> 1357  
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<220>  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1357  
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1 5 10

<210> 1358  
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<222> (7)...(0)  
<223> cSNP translation

<400> 1358  
Lys Pro Ile Thr Arg Lys Gly Val Gly His Arg Met Gly Gly

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&lt;210&gt; 1359

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (7)...(0)

&lt;223&gt; cSNP translation

&lt;400&gt; 1359

Arg Ser Cys Ser His Pro Ser Gln Leu His Arg Leu Val Phe  
1 5 10

&lt;210&gt; 1360

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (7)...(0)

&lt;223&gt; cSNP translation

&lt;400&gt; 1360

Ala Gly Thr Tyr Pro Arg Arg Glu Glu Tyr Arg Arg Gly Ile  
1 5 10

&lt;210&gt; 1361

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (7)...(0)

&lt;223&gt; cSNP translation

&lt;400&gt; 1361

Thr Ile Ser Pro Leu Thr Leu Val Ser Val Ser Pro Ala Asn  
1 5 10

&lt;210&gt; 1362

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (7)...(0)

&lt;223&gt; cSNP translation

&lt;400&gt; 1362

Met Gly Ser His Glu Pro Met Ile Ser Pro Leu Thr Pro Val  
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<210> 1363  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (8)...(0)  
<223> cSNP translation

<400> 1363  
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<210> 1364  
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<212> PRT  
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<220>  
<221> VARIANT  
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<223> cSNP translation

<400> 1365  
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<210> 1366  
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<212> PRT  
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<400> 1366  
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<210> 1367  
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Pro Gly Asn Asn Arg Lys Cys Met Asn  
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<210> 1368  
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<400> 1368  
Ser Val Gly Ala Leu Glu Ala Asn Ser Arg Arg Lys Leu Ala  
1 5 10

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<210> 1370  
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<210> 1371

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<400> 1371  
Ile Glu Thr Tyr Phe Ser Lys Thr Thr Lys Thr Met Ser Ile  
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Pro Leu Ser Gly Ala Leu Ala Gln Ser Leu Arg Pro Ser Lys  
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<400> 1373  
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<210> 1374  
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<400> 1374  
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<210> 1375  
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<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1387  
Asp Lys Ala Glu Lys Thr Lys Lys Lys Lys Lys Lys Arg Lys  
1 5 10

<210> 1388  
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<212> PRT  
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<220>  
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<400> 1388  
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1 5 10

<210> 1389  
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<210> 1390  
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<400> 1390  
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<210> 1391  
<211> 14  
<212> PRT  
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<222> (8)...(0)  
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Tyr Ile Asp Ile Gln Leu Arg Leu Leu Pro Ser His Arg Thr  
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<210> 1396  
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<210> 1397  
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Gly Val Ser Gly Val Lys Pro Gln Gly  
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<223> cSNP translation

<400> 1398  
Leu Lys Pro Val Pro Val Gly Lys Arg Thr Arg Ala Ser Ser  
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<210> 1399  
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<400> 1403  
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<210> 1404  
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<223> cSNP translation

<400> 1404  
Leu Val Lys Leu Lys Leu Lys Lys Ile Pro Trp Met Thr Phe  
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<210> 1405  
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Ser Asn Ser Ile Ser Val Met Gly Val Ser Arg  
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<210> 1406  
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<212> PRT  
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<220>  
<221> VARIANT  
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<223> cSNP translation

<400> 1406  
Thr Glu Trp Ser Gln Trp Ser Asn Val Thr Ser His Val Gly  
1 5 10

<210> 1407  
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<212> PRT  
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<220>  
<221> VARIANT  
<222> (8)...(0)  
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<400> 1407  
Tyr Arg Arg Gln Gly Leu Pro Ile Thr Ile Gly Glu  
1 5 10

<210> 1408  
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<212> PRT  
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<400> 1408  
Val Gly Asp Ala Cys Asp Ser Ala Leu Lys  
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<210> 1409  
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<222> (7)...(0)  
<223> cSNP translation

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<210> 1410  
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<222> (7)...(0)  
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<400> 1410  
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<210> 1411  
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<220>  
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<222> (7)...(0)  
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<400> 1411

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Phe Gly Phe Ser Ser Gly Pro Ser  
1 5 10

<210> 1412  
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<213> Homo sapiens

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<221> VARIANT  
<222> (10)...(0)  
<223> cSNP translation

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Pro Glu Lys Gln Leu Val Glu Lys Lys Val Leu Thr Lys Gln  
1 5 10

<210> 1413  
<211> 13  
<212> PRT  
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<220>  
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<222> (9)...(0)  
<223> cSNP translation

<400> 1413  
Val Val Val Met Gly Pro Pro Lys Leu Glu Arg Ala Leu  
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<210> 1414  
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<212> PRT  
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<220>  
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Phe Ser Glu Asp Asp Pro Trp Arg Pro Leu Ser Ile Gly Pro  
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<210> 1415  
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<212> PRT  
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<223> cSNP translation

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&lt;210&gt; 1416

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (8)...(0)

&lt;223&gt; cSNP translation

&lt;400&gt; 1416

Asn His Met Val Gln Gln Asp Ile Ser Pro Arg Pro Leu His  
1 5 10

&lt;210&gt; 1417

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (8)...(0)

&lt;223&gt; cSNP translation

&lt;400&gt; 1417

Lys Trp Pro Thr Leu Gln Asp Trp Pro Val Leu Pro Trp Arg  
1 5 10

&lt;210&gt; 1418

&lt;211&gt; 14

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (7)...(0)

&lt;223&gt; cSNP translation

&lt;400&gt; 1418

Phe Val Gly Arg Phe Phe Arg Ala Thr Met Ala Thr Gln Leu  
1 5 10

&lt;210&gt; 1419

&lt;211&gt; 9

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (9)...(0)

&lt;223&gt; cSNP translation

&lt;400&gt; 1419

Gln Ile His Arg Ile Arg His Phe Thr  
1 5



<210> 1420  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1420  
Thr Leu Glu Glu Gly Asn Gln Gln Thr Arg Ser Pro Val Pro  
1 5 10

<210> 1421  
<211> 14  
<212> PRT  
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<220>  
<221> VARIANT  
<222> (8)...(0)  
<223> cSNP translation

<400> 1421  
Ala Thr Leu Glu Glu Gly Asn Gln Gln Thr Arg Ser Pro Val  
1 5 10

<210> 1422  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1422  
Ile Leu Asn Gln Pro Thr Leu Arg Leu Leu Pro Met Pro Glu  
1 5 10

<210> 1423  
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<212> PRT  
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<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1423  
Val Asn Cys Ser Ala Val Cys Ala Ser Ser Ser Val Pro Cys  
1 5 10

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<210> 1424  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1424  
Ala Ala Pro Leu Lys Ile Lys Leu Ile Ser Met Arg Leu Gln  
1 5 10

<210> 1425  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1425  
Glu Glu Val Glu Glu Glu Gly Glu Lys Arg Met Phe Ser Pro  
1 5 10

<210> 1426  
<211> 14  
<212> PRT  
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<220>  
<221> VARIANT  
<222> (9)...(0)  
<223> cSNP translation

<400> 1426  
Arg Val Gly Thr Pro Ser Gln Gly His Phe Phe Glu Gly Ala  
1 5 10

<210> 1427  
<211> 14  
<212> PRT  
<213> Homo sapiens

<220>  
<221> VARIANT  
<222> (8)...(0)  
<223> cSNP translation

<400> 1427  
Pro Cys Ala Val Leu Arg Pro Leu Gly Leu Trp Ser Pro Ser  
1 5 10

<210> 1428

<211> 14  
<212> PRT  
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<220>  
<221> VARIANT  
<222> (7)...(0)  
<223> cSNP translation

<400> 1428  
Leu Gly Tyr Thr Pro Gln Arg Pro Val Lys Cys Ala Ser Cys  
1 5 10

<210> 1429  
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<212> PRT  
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<221> VARIANT  
<222> (9)...(0)  
<223> cSNP translation

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Phe Gln Ala Ala Ile Glu Lys Lys Asn Ser Cys Ile Ser Thr  
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Glu Pro Leu Glu Met Ala Arg Pro Leu Ala His Pro Val Ala  
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Arg Leu Asp Arg Glu Arg Lys Lys Asp Lys Asn Glu Arg Gly  
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Asp Ile Ser Ile Cys Gln Glu Cys Pro Ala Trp Arg  
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Ser Thr Ala Leu Arg Ala Asp Ser Thr Gly  
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Tyr Arg Gln Val Asp His Phe Pro Gln Ile His  
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Thr Ile Lys Ser Ala Val Ala Ser Gly Ile Ser Leu Pro Arg

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Pro Asp Arg Val Gly Arg Gln Ser Leu Lys Ser Ser Leu Glu

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<400> 1455

Val Cys Thr Ala Arg Ser Pro Ser Val Arg Ser Ala Arg Ser

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Asn Gln Glu Gly Asp Phe

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1 5 10

<210> 1458  
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Ser Val Gln Arg Val Arg Gln Ser Val Lys Asn Leu Ile Lys  
1 5 10

<210> 1459  
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<400> 1463  
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<210> 1464  
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<400> 1464  
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<210> 1465  
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